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09 828302
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TI Protein and cDNA sequence of Physcomitrella patens signal transduction stress-related proteins and uses in plants for increased tolerance to environmental stresses

IN ***Da Costa e Silva, Oswaldo***; ***Bohnert, Hans J.***; ***Van***

*** Thielen, Nocha***; ***Chen, Ruoying***; ***Ishitani, Manabu***

PA BASF Plant Science G.m.b.H., Germany

SO PCT Int. Appl., 101 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 5

PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 2001077355 A2 20011018 WO 2001-US11398 20010406

TI Moss genes from ***Physcomitrella*** ***patens*** encoding proteins involved in the synthesis of carbohydrates

IN Lerchl, Jens; Renz, Andreas; Ehrhardt, Thomas; Reindl, Andreas; Cirpus, Petra; Bischoff, Friedrich; Frank, Markus; Freund, Annette; Duwenig, Elke; Schmidt, Ralf-Michael; Reski, Ralf

PA Basf Plant Science G.m.b.H., Germany

SO PCT Int. Appl., 133 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 2001044476 A2 20010621 WO 2000-EP12697 20001214

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STIC-Biotech/Ch mLib

∘⊂rom:

∷⊇nt:

abject:

Collins, Cynthia Friday, June 14, 2002 6:07 PM STIC-Biotech/ChemLib sequence search request SN 09/828302

Please search, both prior art and interference, for SN 09/828302:

1) SEQ ID NO:9 2) SEQ ID NO:14

Thank You,

Cynthia Collins Art Unit 1638 CM1, 9A12 (office) or 9E12 (mailbox) (703) 605-1210

> no aut @ 100% FD. 4/6/01 Prov 4/7/00 1026 A/7/99

C L	Sheppard
Searcher: _	
Phone:	- rei: 308-44 99 -
Location:	
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TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(v	where applic.)
STN:	
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Questel/Orbit: _	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

		,		

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Database

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SM Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
E (Dasses 14.799)
Nielsen, K.L. Crockshanks, M., Emmersen, J. and Wellinder, K.G.
EST-sequencing of mature potato tuber (var. Kuras)
Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 98181808
        BE655584 NEOBOROND
BG647922 EST509541
BI667922 EST509541
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115F11 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
sequence.
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Sequenced from the 5' end.
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ORIGIN
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                       13736207 seqs, 6748477542 residues
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                                                       nucleic search, using sw model
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Listing first 45 summaries
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Match Length
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Score

Result

245.6

229 203.4 205.8 196.8 191.6 186.2 186.2 187.2 177.2 175.4 175.4 175.4 175.4

Score 245.6; DB 10; Length 799;

Query Match

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636 691

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XhoI; The CDNA library was constructed from mRNA isolated
from mature flowers of field grown plants for the cultivar
Raiden. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
CDNA fragments were directionally cloned into the
ECORI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GlbcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 316 286 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss41g11.yl Gm-c1061 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1061-1141 5' similar to TR:Q9SZ53 Q9SZ53 PROTEIN PHOSPHATASE 2C-LIKE PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots;
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Beck, C., Yr., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            э;
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van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes Unpublished (2000)
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries Division tell 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGGTCATGGAGGTAAGGCGGTTGCAAAGTTTTGTGCCAAGCACCTTCACCAACAGGTG 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gatggtcacggaggtaaattggtggcaaaattttgtgcaaagcacttacaccaagaggtt 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pBluescript SK(-); Site_1: EcoRI;
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Pred. No. 2.7e-49;
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59.0%;
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Length 577;

Gm-c1061-1341"

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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington Dilversity School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Exa: 314 286 1800
Fax: 314 286 1800
South Memorial Parkway Huntsville, AL 35801 For further information
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
1: 40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sag54a02.yl Gm-c1082 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1082.28 5' similar to TR:Q9SZ53 Q9SZ53 PROTEIN PHOSPHATASE 2C-LIKE PROTEIN.;, mRNA sequence.
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/tissue_type="Roots of bulked Minsoy x Noir RI progeny"
/lab_host="DH108"
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268 TGAGGTTGAGAAAAGACAGGATTCTAAAAGCTGGCGGTTTCATCCAAGTTGGACGAGTCAA 327
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                                                                                                                                                                                                                                                  cggggatgaatttatcgtgctggcctgtgatggata-tgggatgttatgtctagtcaag 917
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/organism="Glycine max"
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1 (bases 1 to 704)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
                                                         EST 18-JUL-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Irradiated Medicago truncatula cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: May GD ...
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238;
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/db_xref="texaon:3880"
/clone="RF016C081R"
/clone_lib="Irradiated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gdmay@noble.org
Insert Length: 704 Std Error: 0.00
Plate: 016 row: c column: 08
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualiflers
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NF016C08IR 5', mRNA sequence.
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Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
Center for Medicago Genomics Research
Unpublished (2000)
into Stratagene's pBluescript II XR Predigested vector (PBLuescript II SK+) vector that has been digested with ECORI and XhoI, and phosphorylated by Stratagene). This library was constucted in the laboratory of Dr. Paul Kelm and Dr. Virginia H. Coryell at Northern Arizona University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula
Ekaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NF084G11EC1F1086 Elicited cell culture Medicago truncatula cDNA clone NF084G11EC 5', mRNA sequence.
BF650146
BF650146.1 GI:11915276
                                                                                                                                                                                                                                                                                                                                     CACACAATITGICCAAGGACCACAAACCIGAACIIGAGGCIGAGAAAGACAGGAITCIA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           704
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                                                                                                                                               497;
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7302
                                                                                                                                              10;
                                                                                                                                            Score 186.2; DB 10
Pred. No. 1.1e-41;
0; Mismatches 183;
                                                                                                                                            Query Match
13.8%;
Best Local Similarity 61.8%;
Matches 296; Conservative
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                                                                                      144
                                                                                                                                            Query Match
Best Local
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                                                                                    BASE COUNT
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Email: radixon@noble.org
Insert Length: 664 Std Error: 0.00
Plate: 084 row: G column: 11
Seq primer: TCACAGGARAACGCTATGAC.
Location/Qualifiers
J. .664
Corganism="Medicago truncatula"
/db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="NF084G11EC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AATGACCGTCTTAGATATGGTTTATCATCAATGCAAGGCTGGCGTGCATCAATGGAAGAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 gcacacaaagctatcttaaacgttgataagaacacgtcaacatcaatatttggcatctt 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gacgaaagtgattattcctatgctgtgctaactgaaagcaatgatagtaacttggccact
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Pred. No. 2.2e-41;
0; Mismatches 264; Indels
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Best Local Similarity 57.0%;
Matches 398; Conservative (
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us-09-828-302-9.rst

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XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE021852 478 bp mRNA linear EST 03-DEC-2001 sm63c10.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-8587 5' similar to TR:081716 081716 PROTEIN PHOSPHATASE 2C
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 ctggattactgcttgtccccaaccaccgccagcaagaaggatgtgataacatgagcatc 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtggctctgattcgtggcaataaactgttcgtcgcaaacgctggagactctcgctgcata 625
                                                                                                                                                                                                                                                                                                                                                                                                                                          686 gagaggaaaaggatagagagtgctggaggcttcgtccatggtggtcgtgttaacggtagt 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 GATTTAGTTCATGAACAACTGTGTTCGGAAACGAGACTTTCTACAGTGTGTGAAAGAGTA 425
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                                                                                                                                                                                                                                                                                                                                                                                                                626 atgicticgacgigggggggggtgtaaatcictcgattgatcacaaacccaacctagagcat 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctaaatcttacaagagcaataggggacatggaattcaagggtcgacctgatttgccacct 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 GAAAAGCAAGTTGTAACTGCCAATCCAGATATAAACACTGTTGAGCTTTGTGATGAAGAT 305
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                                                                                                                                                                                                                                                                                                                                                                7 GTTGCAGTTATTAGAAACAACCAAGTTGTTGTTGCAAATGCTGGTGATTCCCGTTGTGTA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 TTAAACCTTGCAAGAGCTATTGGTGACATGGAATTTAAACAGAATAAGTTTCTTCCCGCT
                                                                                                                                                                                                                                    Length 493;
                                                                                                                                                                                                                             Score 181.6; DB 10; Length
Pred. No. 2.2e-40;
0; Mismatches 184; Indels
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BE021852
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                                                                                                                                                                                                                                13.5%;
62.1%;
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//issue_ins_"an-ciuza"
//issue_ins_"an-ciuza"
//lab_host="Delion"

                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1155 Std Error: 0.00
High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-8587"
/clone_lib="Gm-c1028"
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Pred. No. 3.8e-39;
0; Mismatches 169;
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ity School of
   Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Publi
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62.2%;
                                                                                                       Public Soybean EST
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Matches 278; Conservative
                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                            RESULT 1
BG587548
                                                                                                                                          VERSION
KEYWORDS
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XhoI; Immature pods, ranging in age from 15 to 30 days
after pollination, were collected from greenhouse-grown
plants. At harvest, seeds were removed from pods and
isolated pod walls were collected and immediately frozen
in liquid nitrogen. Pod walls were pooled for mRNA
extraction. CDNA was prepared from polyA+ enriched RNA.
The CDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propogated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                              /tissue_type="immature pod walls"
/dev_stage="immature pods, ranging in age from 15 to 30
days after pollination"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 TGAGGTTGAGAAAGACAGGATTCTAAAAGCTGGCGGTTTCATCCAAGTTGGACGAGTCAA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gocacctgacaagcaagtagtgacgtgctgtcccgatgttgtcgaagttgaccttggacc 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 GCCTGCTGAAAAGCAGGTTGTGACTGCTGATCCTGACGTAACTTCCGTTGAGCTTTGCAA 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 516;
                                                                                                                                                        TIGR sequence name: MTORAO5TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualiffers
1. 516
/cuganism="Medicago truncatula"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%; Score 175; DB 10; Length 5 60.3%; Pred. No. 1.7e-38; Live 0; Mismatches 190; Indels
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
IIO Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
                                                                                                                                                                                                                                                                                          /db_xref="taxon:3880"
/clone="pGPOD-1A9"
                                                                                              Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                /clone_lib="GPOD"
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/ullivary // cultivary // cultivare // wedicago truncatula genotype Al7" // culcae **Pubman*50634" // clone **Libe**NHAM**50634" // clone **Libe**NHAM**50634" // clone **Libe**NHAM**50634" // clone **Libe**NHAM*** // c
                                                                                                                                                                                                                                                                                                       Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Bukaryota: mixed EST libraries.

1 (bases 1 to 638)
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
and Fraser,C.M.
ESTS from roots of Medicago truncatula after colonization with
Glomus versiforme, 2001
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oss pp mRNA linear EST 11-APR-2001 lbbrary cDNA clone pMHAM-50G24 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble Egr name: N36609e TiGR sequence name: MTDDH48TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. 638
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12.7%; Score 171.6; DB 10; Length 638;
Best Local Similarity 57.4%; Pred. No. 1.7e-37;
Matches 371; Conservative 0; Mismatches 239; Indels 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
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Sequence 14,
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-825-855-11
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US-08-935-855-11
US-09-932-463-114
US-09-9244-796-17
US-09-9244-796-17
US-09-9244-796-17
US-09-934-487-2
US-08-909-119-1
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US-09-146-249A-58
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Maximum Match 100%
Listing first 45 summaries
                                      - nucleic search, using sw model
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Maximum DB seq length: 200000000
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1346
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Match Length
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Perfect score:
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Sequence 19, Application US/08935855

GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
TITLE OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNNEY HS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PAtentin Release #1.0, Version #1.30
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%; Score 127.8; DB 3;
59.5%; Pred. No. 1.4e-31;
tive 0; Mismatches 157;
US-08-206-188B-58
US-08-920-812-1
US-08-920-812-1
US-08-920-827-1
US-08-920-827-1
US-08-920-827-1
US-08-920-828-1
US-08-920-828-1
US-08-920-828-1
US-08-446-858-1
US-08-466-1038-5
US-08-466-1038-5
US-08-466-1038-5
US-08-466-1038-5
US-08-469-202-25
US-08-484-434C-33
US-08-484-434C-33
US-08-481-852-20
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   -08-206-188B-58
-08-936-165A-243
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/CONCET WUMBER: 1049-1-002 CIP
TELECHONE: 201-487-5800
TELEPRAN: 201-487-5800
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
LENGTH: 1890 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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Best Local Similarity 59.5
Matches 235; Conservative
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HYPOTHETICAL: NO
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TELECOMMUNICATION INFORMATION:
              TELEPHONE: 201-487-5800
TELEPRAX: 201-343-1684
INPERMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                     LENGTH: 2081 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-935-855-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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SOFTWARE: FastSEC
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CA
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                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              886 tgatggaatatgggatgttatgtctagtcaagctgtcgttgactcgttaaatcaa 941
                                                                                                                                                           3;
                                                                                                                             8.9%; Score 120; DB 3; Length 1824; 57.2%; Pred. No. 4.8e-29; tive 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08935855
Patent No. 606485
GENERAL INFORMATION
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
         STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                             Query Match
Best Local Similarity 57.23
Matches 238; Conservative
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nucleic acid
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STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
                                                                    ; ANTI-SENSE:
US-08-935-855-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-935-855-21
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1271 CCTTCCTGACATCAAGGTGCTGACTCTCAACGACCATGAATTCATGGTCATTGCTTG 1330
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                                                                                           529 agatttccagggtcccatttatgggagtactgcagtggtggctctgattcgtggcaataa 588
                                                   Gaps
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                                                                                                                                                                                                                                                                                  aaatctctcgattgatcacaaacccaacctagagcatgagagaaaaggatagagtgc
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                                                 3;
  Length 2081;
Query Match 8.9%; Score 120; DB 3; Length 20 Best Local Similarity 57.2%; Pred. No. 5.2e-29; Matches 238; Conservative 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-873-093-2
US-08-873-093-2
Sequence 2, Application US/08873093
Sequence 2, Application US/08873093
Sequence 2, Application US/08873093
Sequence 3, Application US/08873093
Sequence 2, Application US/08873093
Sequence 3, Sequence 3, Sequence 3, Applicant Corley, Neil C.
APPLICANT Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Incyte Pharmaceuticals, 3174 Porter Drive
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 tgggagtactgcagtggtggctctgattcgtggcaataaactgttcgtcgcaaacgctgg 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               790 acctgatttgccacctgacaagcaagtagtgacgtgctgtcccgatgttgtcgaagttga 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    637 ACGIGITAATGGTTCATTAGCAGTATCTCGTGCTCTGGGGGACTATGATTACAAGTGTGT 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 817 TAATGAGGAGCTCTGTGAATATGTTAAATCTAGGCTTGAGGTATCTGATGACCTGGAAAA 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2268;
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Pred. No. 2.5e-22;
0; Mismatches 219; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-885-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
TYPE: nuclet acid
TYPE: nuclet acid
TYPE: nuclet acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        970 tttgtgtgaggagatactggattactgctt 999
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.3%;
Matches 231; Conservative (
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                   ; LIBRARY: 13177; CLONE: THPIPLB01
US-08-873-093-2
                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-08-232-463-14/C
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278 tctgaagcgtacgctaaaggtgacttaaaagcaagtttggaatattcctttttacggatg 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 cataaatattcagatttccagggtcccatttatgggagtactgcagtggtggctctgatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7218;
                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.1%; Score 55.8; DB 1;
Best Local Similarity 7.8%; Pred. No. 1e-07;
Matches 33; Conservative 213; Mismatches 175;
                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORREY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
Foley & Lardner
00 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                         COMPUTER READABLE FORM:
BEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703)663-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
                                    Alexandria
                                                                       COUNTRY: USA
ZIP: 22313-0299
                1800
                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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1179 ttcttgtcatgtccaacttctacctaatttcgaatttcaaagacttaaatataaaccta 1238
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                                          Patent No. 6133506
GENERAL INFORMATION:
APPLICANT: Tvpfer, R., Bautor, J., Bothmann, H., Filsak, E., APPLICANT: Hvricke-Grandplerre, C., Klein, B., Martini, N., APPLICANT: M ller, A., Schulte, W., Voetz, M., Walek, J., APPLICANT: Schell, B. Fomoters
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.7%; Score 36.4; DB 3; Length 2750; Best Local Similarity 55.6%; Pred. No. 0.13; Matches 70; Conservative 0; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,860B
FILING DATE: 01-MAR-1996
FILING DATE: 01-MAR-1994
APPLICATION NUMBER: DE P4329951.2
FILING DATE: 05-SEP-1994
APPLICATION NUMBER: DE P4329951.2
FILING DATE: 06-SEP-1993
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2750 Base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: IBM Compatible
                                                                                                                                                                                                                                       ADDRESSEE: Steinberg, Raskin & Davidson, P.C. STREET: 1140 Avenue of the Americas CITY: New York
                     Sequence 33, Application US/08617860B Patent No. 6133506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 17, Application US/09007005B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cuphea lanceolata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Cuphea lanceolata IMMEDIATE SOURCE:
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LOCATION: 2637..2750
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                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                        New York
: USA
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US-08-617-860B-33
  US-08-617-860B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-007-005-17
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Pred. No. 2.7e-06;
0; Mismatches 63; Indels
                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Griley, Neeti
APPLICANT: Grolley, Neil C.
APPLICANT: Ghah, Purvi
TILE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     764 atagggacatggaattcaagggtcgacctg 794
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                                                                                                         Sequence 10, Application US/09013881
Patent No. 6132964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME:
BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: 9F-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
METEREAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.7%;
Best Local Similarity 58.3%;
Matches 88; Conservative
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US-09-013-881-10
                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                            RESULT 7
US-09-013-881-10
1046 G 1046
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RESULT

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FEATURE:
OTHER INFORMATION: Translation template
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CORRESPONDENCE ADDRESS:
ACRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-022-461-1/c
; Sequence 1, Application US/09022461
; Patent No. 5964371
                                                                                                                           NAME/KEY: misc_feature
CATTON: (1)...(289)
COTHER INFORMATION: n = A,T,C or
US-09-244-796-17
          TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 415-813-5600
415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPANNE: 415-813-560
TELEFAX: 415-494-0792
TELEX: 70614
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 755 PAGE
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 nrsrnrnsrnrrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 gagatgatgaagggagcaagtgggtggaaagagcttcaaagtttggaggaaacaagtagt 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 nrsrnrnsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnr 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 grarcrararururarcrurarurururarcrararururarcrararurgrnrnrsrnr 65
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Sequence 17. Application US/09244796
Sequence 17. Application US/09244796
Sequence 17. Application US/09244796
Sequence 18. Septicant 18. Settle New Title OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: 1995-00-05
SEARLIER FELICATION NUMBER: 60/035,963
EARLIER PILING DATE: 1999-01-05
SEARLIER FILING DATE: 1999-01-11-06
SEARLIER PILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastERED for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
GENERAL INFORMATION:
APPLICANT: SOStak, Jack W.
APPLICANT: SOStak, Jack W.
APPLICANT: SOSTAK, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: EVISIONS
TITLE REPERRACE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER PELING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 17
EFFORMARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.6%; Score 35; DB 4; Length 289; Best Local Similarity 7.3%; Pred. No. 0.099; Matches 17; Conservative 94; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANIZAR: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(289)

UCHER INFORMATION: n = A,T,C or
US-09-007-005-17
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221 ggaggtaaattggtggcaaaattttgtgcaaagcacttacaccaagaggttctgaagtct 280
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                                                                                                                                                                                                                                                                                                                                        341 gagatgatgaagggagcaagtgggtggaaagagcttcaaagtttggaggaaacaagtagt 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.6%; Score 35; DB 4; Length 289; Best Local Similarity 7.3%; Pred. No. 0.099; Matches 17; Conservative 94; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

GREAT APPLICANT: HENDERSON, Daniel R.

APPLICANT: SCHUUR, Eric R.

APPLICANT: LAMPARSKI, Henry G.

APPLICANT: YU, De Chao

TITLE OF INVENTION: PROSTATE CANCER DRUG SCRE

TITLE OF INVENTION: ENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,461
FILING DATE: 12-FEB-1998
CCASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 06/906,192
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20003.21
TELECOMMUNICATION INFORMATION:
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686 ARGARGARAAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGARGARGARGARGATNTTYGAYG 745
                                                                                                                                                           216 gtcacggaggtaaattggtggcaaaattttgtgcaaagcacttacaccaagaggttctga 275
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                                                                                                                   746 AYGARGAYGARGARGARAAYATHGARWSNAARGTNACNAARCCNGTNCARATHCARA
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                                                                                336 tggatgagatgatgaagggagcaagtgggtggaaagagcttcaaagtttggaggaaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

2.4%; Score 32.8; DB 1;
Best Local Similarity 26.3%; Pred. No. 1.7;
Matches 69; Conservative 53; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08676974
Patent No. 5770422
GENERAL INFORMATION:
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10°
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICAL:
FILING DATE:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSMIND Ph.D., Richard A
RESISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-
TELECOMMUNICATION INFORMATION:
"FURPHONE: (415)343-4341
                                                                                                                                                                                                                                    456 aaagtgattattcctatgctgt 477
                                                                                                                                                                                                                                                                        866 AYYTNGARGARWSNGAYWSNAT 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)343-4342
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTR: ...
ZIP: 94104
COMPUTER READABLE FORM:
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CITY: San Francisco
STATE: CA
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; MOLECULE TYPE:
US-08-676-974-2
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US-08-676-974-2
      276
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                                                                                                                                                                             Gaps
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0
                                                                                                                                     Length 12047;
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                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.4%; Score 32.8; DB 1; 1
Best Local Similarity 26.3%; Pred. No. 1.7;
Matches 69; Conservative 53; Mismatches 140;
                                                                                                                                                                           59;
                                                                                                                                   Score 33.6; DB 2;
Pred. No. 2.5;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08676967
Patent No. 5747317
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                   2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARGERISTICS:
LENGTH: 2277 base pairs
; LENGTH: 12047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLGX: linear
US-09-022-461-1
                                                                                                                             Query Match
Best Local Similarity 53.9<sup>5</sup>
Matches 69, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      3682 TGGTTTCT 3675
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US-08-676-967-2
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US-08-676-967-2
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Gaps

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Length 2277; Indels œ

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866 AYYTNGARGARWSNGAYWSNAT 887
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US-08-118-469A-1/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               746 AYGARGAYGARGARGARAAYATHGARWSNAARGTNACNAARCCNGTNCARATHCARA 805
                 216 gtcacggaggtaaattggtggcaaaattttgtgcaaagcacttacaccaagaggttctga 275
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; Pred. No. 1.7;
53; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/098,487
                                                                                                                                                                                                                                         Sequence 2, Application US/09098487
Patent No. 5917025
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING JOILE.

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMEAN Ph.D., Richard A
REGIGTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 0C896-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERIFICS:
LENGTH: 2277 Dase pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                   456 aaagtgattattcctatgctgt 477
                                                                                                                                          866 AYYINGARGARWSNGAYWSNAT 887
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Best Local Similarity 26.3%;
Matches 69; Conservative 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: CDNA US-09-098-487-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94104
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                                   GENERAL INCRMATION:
APPLICANT: Flavell, Richard A.
APPLICANT: Flavell, Richard A.
APPLICANT: Fikrig, Erol
APPLICANT: Kantor, Fred S.
APPLICANT: Mantor, Fred S.
APPLICANT: Barthold, Stephen W.
TIFLE OF INVENTION: NOVEL B. BURGDORFERI POLYPEPTIDES
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: LOSAM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,469A
FILING DATE: 08-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/099,757
FILING DATE: 30-ULL-1993
ATTONNEY/AGENT INFORMATION:
ANALY: ASSETT THEOREMATION:
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1207 ttcgaatttcaaaagacttaaatataaa 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: YU-1C
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 596-900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1498 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 60.29
Matches 53; Conservative
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CITY: New York
STATE: New York
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COUNTRY: U.E
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LOCATION:
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US-08-118-469A-1
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Search completed: June 19, 2002, 19:49:52 Job time: 4028 sec

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Perfect score:

Sequence:

OM nucleic

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Human immune/haema
Protein phosphatas
Drosophila melanog
Drosophila melanog
Arabidopsis thalia
Arabidopsis thalia
Breast cancer asso
Mouse ischaemic co
Mouse magnesium-de
Human secreted pro
Human nervous syst
Human reproductive
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Protein phosphatas
Drosophila melanog
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DNA encoding novel
Human MP-19 partia
Cat flea hindgut a
           Zea mays DNA fragm
Human MP-19 full l
                              Drosophila melanog
FIN13 serine/threo
                                                 Drosophila melanog
Zea mays DNA fragm
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Drosophila melanog
Human protein phos
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Lambda SL9-1 clone
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ABL02369
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ABL01567
ABA15878
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AAK85395
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99US-0123548.
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99US-0126785.
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99US-0127462.
99US-0127462.
99US-012814.
 2000EP-0301439
Arabidopsis thaliana
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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                                                               June 19, 2002, 18:43:49; Search time 210.22 Seconds
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                              lotal number of hits satisfying chosen parameters:
                                                                                                                                                                             1736436 seqs, 858457221 residues
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                                             nucleic search, using sw model
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Score

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99US-0123180.
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59.2%; Pred. No. 3.4e-91;
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872 atcgtgcttgcctgtgatggaatatgggatgttatgtctagtcaagctgtcgtggacttc 931
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                                                               gttaaatcaagattacctaccaccaaaactctatcatcttgtgtgaggagatactggat
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4.1e-84;
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990S-0161404.
990S-0161405.
990S-0161406.
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979 ggagatactggattactgcttgtccccaaccacccgccagcaagaaggatgtgataacat 1038
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                                                                                                                                                                                                                                                                                                 900 atgitaigictagicaagcigicgiggacticgitaaaicaagaitacciaccaccaaaa 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 actgcatgtcaagccagccagttggtcgatttcatccgcgagcatatagacacagaggaaa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 gcctctcggcagtatgcgagagagtgctcgatagatgcctggctccgtcgaccatgggcg 420
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    tcaagggtcgacctgatttgccacctgacaagcaagtagtgacgtgctgtcccgatgttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                               840 tcgaagttgaccttggacccgggggatgaatttatcgtgctggcctgtgatggaatatggg
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                                                                                                                                                               11.6%; Score 155.6; DB 21; Length 467; 58.4%; Pred. No. 2.3e-38; ive 0; Mismatches 194; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 gcgagggatgcgataacatgacgatgatcctggttcagttcaagaa 466
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99US-0123180.
99US-0123548.
99US-0161404.
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99US-0161992.
99US-0161993.
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                                                                                                                                                                                            Matches 272; Conservative
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05-MAR-1999;
09-MAR-1999;
25-OCT-1999;
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26-OCT-1999;
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                                                                                                                                                                                                                                                        Length 449;
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Pred. No. 3.4e-38;
2; Mismatches 177; Indels
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990S-0158029.
990S-0158232.
990S-0159293.
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990S-0159638.
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59.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing secretion of heterologous proteins e.g. lipase and cellulase in eukaryotic cells useful in industry to increase production and facilitate purification, by inducing an elevated unfolded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 ctggagactctcgctgcataatgtctcgacgtggcgaggctgtaaatctctcgattgatc 665
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|||| || || || || || || || || || || acaagcctcagcttggcggtttcgtcgact 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 tttatgggagtactgcagtggtggctctgattcgtggcaataaactgttcgtcgcaaacg 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                         Ptc2; phosphatase; unfolded protein response; protein secretion;
                                                                      Trichoderma reesei Ptc2, involved in unfolded protein response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valkonen MJ, Saloheimo MLA;
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Pred. No. 5e-35;
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                                                                                                                                                                                             Location/Qualifiers
237..1553
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                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09401
                                                                                                                                                                                                                                                                                                                                                                              24-MAR-2000; 2000US-0534692
                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ward M,
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                                                                                                                                                               Trichoderma reesei,
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                                  21-DEC-2001
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AAH26935;
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Increasing secretion of heterologous proteins e.g. lipase and cellulase in eukaryotic cells useful in industry to increase production and facilitate purification, by inducing an elevated unfolded protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             961 aatcttcccaggctgttgttgagtttgtgcgacgaggcatcgccgccaagcaggaccttg 1020
846 ttgaccttggacccgggggatgaatttatcgtgcctgtgatggaatatgggatgtta 905
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                                                                                                                                                                                                           841 agagcgccgagctgtcccccgaaaaccagatcgttaccgcctttcccgatgtcgaggtgc
                                                                                                                                                                                                                                                                                                                                                                                                                       901 acgagettacagaggaggacgagttcctggtgattgcctgtgacggtatctgggattgcc
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/product= "Ptc2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichoderma reesei ptc2 cDNA.
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P-PSDB; AAE15376.
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23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
11-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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                                   Ouery Match 10.8%; Score 146; DB 24; Length 1824; Best Local Similarity 57.1%; Pred. No. 5e-35; Matches 266; Conservative 0; Mismatches 200; Indels 0
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        Sequence 1824 BP; 429 A; 524 C; 512
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0; Mismatches 168; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is a sering-threonine phosphatase derived from human placenta. The nucleic acid sequence encodes a human protein phosphatase of the protein serine/threonine phosphatase family and is of the prot class which are regulate in the regulation of fatty acid and cholesterol biosynthesis. The MP-19 protein is useful in the treatment of leukaemia, brain, prostate and breast cancer, Alzaheimer's, Huntington's or Parkinson's diseases, epilepsy, reproductive disorders and regulation of spermatogenesis or maturation of mammalian germ cells.
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phosphorylation dependent disease; leukaemia; breast; brain;
prostate; epilepsy; fatty acid; cholesterol; ds.
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                                                                                            Homo sapiens
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                               SEQ ID NO 10163.
                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                    pharmaceutical; gene; ss.
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                                              ABL05227 standard;
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WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the coding sequence for the protein of the invention. The protein of the invention is a fibroblast growth factor-inducible protein (FIN13) serine/threonine phosphatase, which has a collagen-homology domain, an acidic box, a serine/threonine phosphatase domain and a charged domain characteristic of a putative nuclear localisation sequence. A host cell transformed with this sequence is used for the recombinant production of FIN13. A vector containing this
                                                                                                                           atctttgtgtgaggagatactggattactgcttgtcccc---aaccacccgccagcaaga 1023
gaacgtaaccctaccagctgaggaacaaatgatatctgccctacctgacataaagaagct 1754
                                                                                                                                                                                                                                                                                                                                                   FIN13; serine/threonine phosphatase; hyperproliferative disorder; fibroblast growth factor-inducible protein; collagen-homology domain; uncontrolled proliferation; neoplasm; tumour; therapy; ds.
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                                                                                  tgaccttggacccgggggatgaatttatcgtgctggcctgtgatggaatatgggatgttat
                                                                                                                tcgacctgatttgccacctgacaagcaagtagtgacgtgctgtcccgatgttgtcgaagt
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                                                                                                                                                                                                            FIN13 serine/threonine phosphatase coding sequence.
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sequence can be used to increase the level of expression of FIN13, especially to treat a disease or disorder associated with uncontrolled proliferation in an animal. FIN13 can also be administered directly to treat uncontrolled proliferation, e.g. hyperproliferative disorders, neoplasms and tumours. A labelled antibody against the encoded protein, or an antisense oligonucleotide against this sequence can be used to detect and quantitate FIN13 in a biological sample.
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Pred. No. 7.4e-27
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                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

The sequence data for this patent did not form part of the printed specialication, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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                                                                                              Claim 1; SEQ ID NO 10160; 21pp + Sequence Listing; English.
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Sequence Sequence

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Arabidopsis thaliana AT4g31860/F11C18_60 mRNA, complete cds. AY057611 AY057611 GI:16209697 FILC18_50 MRNA, complete cds. FILC_CDNA.
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Arabidopsis thaliana cDNA to mRNA.
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CMTSQQLVDFIHEQINSETKLSVVCEKVLDRCLAPNTSGGEGCDNMTMILLVRFKNPTP
SETELKPBASQAEGNHDEPSSSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Pallm, C.J., Paham, P.K., Quach, H.L., Southwick, A., Theologis, A., and Ecker, J.R.
    Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin Neumann, G.,
Rawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P. K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Direct, Submission
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                                                                                                                                                                                                                                Submitted (20-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                         RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, R. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          goacacaaagetatettaaacgttgataagaacacgtcaacatcaatatttggcatettt 211
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    1531
    /organism="Arabidopsis thaliana"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="AT4g31860/F11C18_60"
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/db_xref="G1:16209698"
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/chromosome="4"
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PLN 13-FEB-2002

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                                                                             Substrate Specificity of Type 2C Protein Phosphatases (PP2C) in Arabidopsis thaliana Unpublished
2 (bases 1 to 1463)
Fukuhara,T.
Direct Submission
Submitted (09-FEB-2002) Toshiyuki Fukuhara, Tokyo Univ. of Agri. 6 Tech., Dept. of Applied Biological Sciences; Saiwaicho 3-5-8, Fuchu, Tokyo 183-8509, Japan (E-mail:füku@cc.tuat.ac.jp, Tel:81-42-367-5622, Fax:81-42-360-8830)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 ATATCGATGGGTACATACCTAAGTTCTCCGAAAACTGAAAAGTTATCAGAAGATGGTGAG 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 GCGCATGCTGCAATTCTTGATCTTGATGATAA-----GACATCGTTCTTCGGTGTGTAT 310
                                         Izumi,S., Yamada,M., Ohsato,H., Miyazaki,S., Bohnert,H.J. and Fukuhara,T.
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               eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="protein phosphatase 2C"
/protein_id="BAB84700.1"
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                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 302; DB 8;
Pred. No. 4.2e-76;
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1522 bp mRNA linear PLN 26-AUG-2001
Arabidopsis thaliana putative protein phosphatase 2C
(F27C12.1/At2g25070) mRNA, complete cds.
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                                                       Submitted (14-JUL-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
Street, Albany, CA 94710, USA
RIKEM Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA: RIKEN expression of Clustering of RAFL CDNAS (RAFL CDNA: RIKEN Satou,M. Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Ishida,J., Hayashizaki,Y. and Shinozaki,K.
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Location/Qualifiers
Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S..
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Direct Submission
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(FLC-1) as a BamHI/XhoI insert.
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/db_xref="taxon:3702"
/chromosome="2"
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Pred. No. 4.2e-76;
0; Mismatches 400;
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                                                                                                                                                              Direct Submission
Submitted (08-DEC-1999) Blochemistry, University of Missouri, 117
Schweitzer Hall, Columbia, MO 65211, USA
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 Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1107)
Broz,A.K., Thelen,J.J., Muszynski,M.G., Miernyk,J.A. and
Randall,D.D.
                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1107;
                                                                  a novel type-2C protein phosphatase from maize Bot. 52 (361), 1739-1740 (2001)
                                                                                                                                       Miernyk, J.A., Muszynski, M.G.
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/protein_id="AAG43835.1"
/db_xref="G1:12003990"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.6%; Score 277.6; DB 8; 56.6%; Pred. No. 4.7e-69; ive 0; Mismatches 419;
Spermatophyta; Magnoliophyta; Lilic
clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
                                                                                                                                                                                                                          1. .1107
/organism="Zea mays"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                  1. .1107
/gene="pp2c-1"
1. .1101
                                                                                                                        2 (bases 1 to 1107)
Broz, A.K., Thelen, J.J.,
Randall, D.D.
                                                                                                                                                                                                                                                                                                          /gene="pp2c-1"
/note="PP2C-1"
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Matches 601; Conservative
                                                                     ZMPP2, a novel
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21372152
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                                         AUTHORS
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1 (sites)
Penttila,M.E., Ward,M., Wang,H., Valkonen,M.J. and Saloheimo,M.I.
Production of secreted proteins by recombinant eukaryotic cells
Patent: WO 0172783-4 9 04-0CT-2001;
GENENCOR INTERNATIONAL, INC. (US)
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Eukaryota, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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                                               575 attogtggcaataaactgttcgtcgcaaacgctggagactctcgctgcataatgtctcga
                                                                                                                           502 GTCAGAAATAGGCAACTCGTTGTGGCAAATGCTGGTGACTCCCGCTGCGTCATCTCAAGG
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                                 aagcataaatattcagatttccagggtcccatttatgggagtactgcagtggtggctctg
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Best Local Similarity 57.1%; Pred. No. 5.7e-31;
Matches 266; Conservative 0; Mismatches 200; Indels
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/organism="Hypocrea jecorina"
/db_xref="taxon:51453"
524 c 512 g 359 t
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AX319337.1 GI:17901129
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AUTHORS
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NLSRAIGDHFYRNKNLPPEECMISALPDIKVLTLTDDHEFWIACDGIWNYMSSQEV
IDFIQSKISQRDENGELRLSSIVEYLLDQCLAPDTSGDGTGCDNMTCIIICFKPRNT
AAPQPESGKRLLESLUSTEGAESONGHSDKKKAKRD"
458 c 587 g 385 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanesystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (01 MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1206 AGACTCCCGCTGTGTGGTGTCTGAGGCCGGCAAAGCTTTAGACATGTCCTATGACCACAA
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                                                                                                                                                                             Length 1919;
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                                                                                                                                                                                                                   0; Mismatches 156;
                                                                                                                                                                             DB 4;
                                                                                                                                                                          Score 129.4; DB 4
Pred. No. 3.6e-26;
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Tissue Procurement: ATCC
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Strausberg, R.
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AUTHORS
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Ab_xref="G1:1754694"

Ab_xref="G1:1754694"

/translation="MGNYLSQPNTVKCSGDGVGASRLPLPYGFSAMQGWRVSMEDAHN

CIQELDSETAMFSVYDGHGGEVALYCAKYLPDIIKDQKAYKEGKLQKALEDAFLAID

AKLTTEEVIKELAQIAGRPFEDEDEKEKVADEDDVDNEEAALLHEEATWIIELLTYK

GQNCHKGAPHSKSGAGTGEEPGSQGLNGEAGPEDPSRETSAEVNGPTAKAHTGLSSNS
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CSEEEDGYSSERAENEEDEDDTEEAEEDDEEEEMMVPGMEGKEEPGSDSGTTAVVALI
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Submitted (05-DEC-1996) Laboratory of Biochemistry, National Heart
Lung and Blood Institute, Bldg 3, Rm 218, 3 Centre Drive, Bethesda,
MD 20892, USA
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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/organism="Bos taurus"
/db_xref="taxon:9913"
/172. .1803
/note="MCPP; Method: conceptual translation with partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         606 ctggagactctcgctgcataatgtctcgacgtggcgaggctgtaaatctctcgattgatc 665
                                                                                                                                                             781 TTGGCCGAGTCAACGGCAATCTGGCTCTGTCGCGTGCCATTGGCGACTTTGAATTCAAGA 840
                                                                                                                                                                                                                                                                                                          786 gtcgacctgatttgccacctgacaagcaagtagtgacgtgctgtcccgatgttgtcgaag 845
                                                                                                                                                                                                                                                                                                                                 666 acaaacccaacctagagcatgagagaaaaggatagagagtgctggaggcttcgtccatg
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                                                                                      661 CCGGTGATTCTCGAAGCGTGCTGGGCATCAAGGACGGGCCAAACCCCTATCCAACGACC
                                                                                                                                                                                                                      726 gtggtcgtgttaacggtagtctaaaatcttacaagagcaatagggacatggaattcaagg
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Huang,C.Y. and Qin,K.
Characteristics of a Mg-dependent, calcium-inhibitable
serine/threonine protein phosphatase revealed by its CDNA
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/codon_start=1
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/TLNL at: http://image.llnl.gov Series: IRAL Plate: 24 Row: 9 Column: 23.
Location/Qualifiers
                                                                                                                                                                                       /codon_start=2
/product="Similar to protein phosphatase 1G (formerly 2C),
magnesium-dependent, gamma isoform"
/protein_id="AAH07361.1"
/db_xref="GI:13938440"
                                                                                                                                                                                                                                                                                            MVPGMEGKEEPGSDSGTTAVVALIRGKQLIVANAGDSRCVVSEAGKALDMSYDHKPED
EVELARIKNAGGKVTMDGRVNGGLNLSRAIGDHFYKRNKNLPPEEQMISALPDIKVLT
LTDDHEFMVIACDGIWNVMSSQEVVDFIQSKISQRDENGELRLLSSIVEELLDQCLAP
                                                                                                                                                                                                                                                                /translation="ARGFSSNSERGTEAGQVGEPGIPTGEAGPSCSSASDKLPRVAKS
KFFEDSEDESDEAEEEEEDSEECSEEEDGYSSEEAENEEDEDDTEEAEEDDEEEEEEM
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                                                                    /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="IMAGE:3627167"
/tissue_type="Brain, neuroblastoma"
/clone_lib="WHH_MGC_19"
/lab_host="nB10B=R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 127.8; DB 9; 59.5%; Pred. No. 1e-25;
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unclassified.
1 (bases 1 to 1641)
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Travis.S.M.

Direct Submission

Submitted (19-JUN-1997) Travis S.M., Internal Medicine, University

of Iowa, 500 EMRB, Iowa City IA 52242 USA

(bases 1 to 1932)

Travis,S.M. and Welsh,M.J.

PP2C gamma: a human protein phosphatase with a unique acidic domain 97420453
                                                                                                                                                                                                                                                                          1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1932)
                                                                                                                                                                                                                                                                                                                                                                                                       1221 AAACAAGAACCTGCCACCTGAGGAACAGATTTCAGCCCTTCCTGACATCAAGGTGCT 1280
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Homo sapiens mRNA for protein phosphatase 2C gamma.
Y13936
                    protein phosphatase
                                                                                                                                                                                                                                    Score 127.8; DB 6;
Pred. No. 1e-25;
0; Mismatches 157;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="Skeletal muscle"
25. .1665
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372 c 500 q 307 t
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Pohl,J.D. and Hanke,M.D.
Nucleic acid encoding a human prote
Patent: EP 0874052-A 3 28-OCF-1998
BIOPH BIOTECH ENTW PHARM GMBH (DE)
Location/Qualifiers
1..1641
                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
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Tissue Producement: ArCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Retteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
  URL: http://mgc.nci.nih.gov
                                                   Email: cgapbs-r@mail.nih.gov
NIH-MGC Project URL: h
Contact: MGC help desk
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GONCHKGPPHSKSGGGTGEEPGSOGLNGEAGPEDSTRETPSQENGPTAKAYTGFSSNS
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CSEEDCYSSERARNEDDDTFEAEDDDFEBEEBMVPGMEGKEPGSDSGTTAVVA
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GINLSRAIGDHFFKRNKLPPEEQMISALDMSYDHKPEDGVELARIKNAGGKVTMOGRVNG
GINLSRAIGDHFFKRNKLPPEEQMISALDGCLAPDTSGDGTGCDNMTCIIICFKPR
NTARLQPESGKRKLEBYLSTEGAEBGNSDKKKKARRD"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2169)
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2169 bp mRNA linear PRI 24-JAN-2C Homo sapiens, protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform, clone MGC:2870 IMAGE:2988852,
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Submitted (22-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1125 ACCAGAGGATGAAGTAGAACTAGCACGCATCAAGAATGCTGGTGGCAAGGTCACCATGGA 1184
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                           /evidence=experimental
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BC022061
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les 235; Conservative
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/product="protein phosphatase 1G (formerly 2C),
magnesium-dependent, gamma isoform"
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magnesium-dependent, gamma isoform"
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/protein_id="
                found
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 3 Row: b Collumn: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1097 TGGTACAACAGCGGTGGTGGCCCTGATACGAGGGAAGCAGTTGATGTAGCCAACGCAGG 1156
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/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
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Pred. No. 1.1e-25;
3; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="LocusID:5496"
/db_xref="taxon:9606"
/clone="MGC:2870 IMAGE:2988852"
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens
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117. .1757
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .2169
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                                         Score 127.8; DB 9;
Pred. No. 1.1e-25;
0; Mismatches 157;
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1. .486
                                         Query Match
Best Local Similarity 59.55
Matches 235; Conservative
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /traislation="MCAYLSOPNTVKCSGDGVGAPRLPLPYGFSAMOGWRVSWEDAHN
CIPELDSETAMFSVYDGHGGEEVALYCAKYLPDIIKDQKAYKEGKLQKALEDAFLAID
AKLITTERVIKELAQIAGRPTEDEDEKEKVADEBDVDVRERAALLHEFRYWTIEELLTRY
GQNCHKGPPHKKSGGGTGEPGSGGLNGEAGPEDSTRETPSQENGFTAKAYTGFSSNS
ERGTFAGQVGERGIPTGEAGPSCSSAADKLFRVAKSRFFEDSEDEREEEDSEE
CSEBEDGYSSEEAENBEDEDDTEEAAEDDFEEEEEMVPGMEGKEEPGSDSGTTAVVA
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GLULSKALGDHFYKRNKNLPPEEQMJASALPDIKVLTLTDDHFEMVIACDGINNVMSSQ
EVUDFIGSKISQRENGELKLISSIVEELLOQCLAPDTSGDGTGCDNNTCIIIGFKPR
NTAELQPESGKRKLEEVLSTEGAEENGNSDKKKKAKRD"
                                                                                                                                                                                                            PRI 12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                     BC000057

Homo sapiens, protein phosphatase 1G (formerly 2C),
magnesium-dependent, gamma isoform, clone MGC:1675 IMAGE:3505271,
                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform" // protein_id="AAH00057.1" // db_xref="G1:12652623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="Locus10:5496"
/db_xref="taxon:9606"
/clone="MGC:1675 IMAGE:3505271"
/tissue_type="Placenta, choriocarcinoma"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                               907 gtctagtcaagctgtcgtggacttcgttaaatcaa 941
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120. .1760
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 2176)
Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1. .2176
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BC000057
BC000057.1 GI:12652622
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BC000057
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                      1340 AAACAAGAACCTGCCACCTGAGGAACAGATTTCAGCCCTTCCTGACATCAAGGTGCT 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                              1100 TGGTACAACAGCGGTGGTGGCCCTGATACGAGGGAAGCAGTTGATTGTAGCCAACGCAGG 1159
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                                                                                                                                                                                                                                                                             1280 TGGGCGAGTCAACGGGGGCCTCAACCTCTCCAGAGCCATTGGGGACCACTTCTATAAGAG
                                                                                                                                                                                                                                                                                                                      787 tegacetgatttgecacetgacaagcaagtagtgaegtgetgteeegatgttgtegaagt
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                                                                                                                                         acccaacctagagcatgagagaaaaggatagagagtgctggaggc---ttcgtccatgg
                                                                                                                                                                                                                                      tggtcgtgttaacggtagtctaaatcttacaagagcaataggggacatggaattcaaggg
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Jiang,Y., Harlocker,S.L. and Secrist,H.
Compositions and methods for the therapy
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CORIXA CORPORATION (US)
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Sequence 2075 from Patent WO0196388.
AX341828.1 GI:18137810
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/db_xref="taxon:9606"
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DLKSSDHKENFKMRSPYFRGRRAAALAAEATNKAVMDPSAKPDGSSTSAAAAAAAAA
DGVANSRNPSNVVNPMAGADSNTTTSINDLSTKNAALKDDSVNDQNEGSNGTDFKHTL
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DNVKSPDTSSARSSDCTENDDGDEDGNEDSDEBETDEDQMANDNFCAMIEBPSKDS
GCTAVCTLGSRASSROCTENDDGDEDGNEDSDEBETDEDQMANDNFCAMIEBPSKDS
GCTAVCLLGGRDLYVANAGDSRCVISRSGQAIEMSIDHKPEDDEBARIIKAGGRVT
LDGRVWGGLNLGRALGHAYKTVUTLAREGQMISALPDIKKLLITPEDBEFWVLACDGI
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/db_xref="GI:15291807"
                       129 CAGGAAGTTGTAGATTTCATTCAATCAA 102
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/codon_start=1
    914 caagctgtcgtggacttcgttaaatcaa
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                                                                                                                                                                                                                                               fruit fly.
Drosophila melanogaster
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734 gttaacggtagtctaaaatcttacaagagcaataggggacatggaattcaagggtcgacct 793
                                                                                                                                                                      244 AACCTGCCACCTGAGGAACAGATGATTCAGCCCTTCCTGACATCAAGGTGCTGACTCT 303
                                                                                                                                                                                                                         854 ggacccggggatgaatttatcgtgctggcctgtgatggaatatgggatgttatgtctagt 913
                                                                                                                                                                                                                                               304 ACTGACGACCATGAATTCATGGTCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGC 363
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                                                                                                                                        794 gatttgccacctgacaagcaagtagtgacgtgctgtcccgatgttgtcgaagttgacctt
                                                                                 794 gatttgccacctgacaagcaagtagtgacgtgctgtcccgatgttgtcgaagttgacctt
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 154;
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AX351366
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Pred. No. 4.1
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/db_xref="taxon:9606"
138 c 111 g 134
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Location/Qualifiers
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les 231; Conservative
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AX351366/c
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into studies was sequenced as part of a might curroughque process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular CDNA clone. However, there are artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to callediting including its location includitiers
                                                                                                                                                                                                                                                                                                                                                                                      Prerygota, Neoptera, Endoptery, Itanian, Presy, Neoptera, Endoptery, Prerygota, Neoptera, Endoptery, Differa, Brachycera, Brachycera, Brachycera, Brachycera, Brachycera, L. (base, M. 2510)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Paragas, V., Parak, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S. B., Rubin, G.M. and Celniker, S. Direct Submission

Submitted (10-AdG-2001) Berkeley Drosophila Genome Project, Berkeley Mational Laboratory, One Cyclotron Road, Berkeley Ca 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720, USA
Sequence Submitted by:
Berkeley, CA 94720 This Sequence of a high-throughput process to
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/db_xref="FLYBASE:FBgn0033021"
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Drosophila melanogaster LD27655 full length cDNA. AY051748 AY051748 GI:15291806 FILCHA
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/product="LD27655p"
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KTDLEQGRIKDRTPESPSNOMEDPTQRAIKEVTIIVSS"
460 c 506 g 673 t
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Eukaryota; Fundi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomyces.
1 (Dases I to 1920)
Shizosaci, x and Russell.
Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase homolog in the osmoregulation of fission yeast
BMBO J. 14 (3), 492-502 (1995)
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Schizosaccharomyces pombe protein phosphatase 2C gene (ptc2+)
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protein phosphatase 2C.
Schizosaccharomyces pombe (strain 972) DNA
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595. .1707
                                                                                          Score 124.6; DB 3;
Pred. No. 9.1e-25;
0; Mismatches 229;
                                                                                            9.3%;
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NTDPDDEFLILLACOFWDGKSSQCWFEVRRGIVARQSLEVTCENLMDRCIASNSES
CGIGCONMTICIVAEHGRGEEDWYNNITQRVNSGEDFOXTARNSES
LQLEYDHIASHEYGSGDTYDSDSDDETIAYDRYYLH"
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Pred. No. 6.6e-24;
0; Mismatches 169;
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/protein_id="AAA67320.1"
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ne: 5807 sec
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Best Local Similarity 56.9
Matches 223; Conservative
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1 MGIYLCSPKTDKTSEDDENA......MSIIIVQPKQSGVAASSSTD 353
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Copyright (c) 1993 - 2000 Compugen Ltd.
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9: sp_phage:*
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11: sp_rodent:*
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æ	Query	54.0	53.0	52.7	35.7	30.4	30.1	29.9	29.7	29.4	29.4	29.4	29.3	29.1	28.3	28.3	27.5
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SUMMARIES

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Q961N7 Q9U5F4 Q43966 Q43966 Q9SU64 Q9SUD2 Q9SLD2 Q9FRJ1 Q9FRJ1 Q9FRJ1 Q9FRJ1 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9LNW3 Q9CND2 Q9	rep p p p p p p p p p p p p p p p p p p	Score 992 Pred. No. 61; Mismat RYGLSAMOGWR :: :
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN PHOSPHARASE 2C-LIKE PROTEIN (AT4G31860/F11C18_60).
F11C18.60 OR AT4G31860.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                     GSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQA 294
                                                                                                                                                                                                      33 LVDFIREHINTEESLSAVCEGVLDRCLAPSTMGGEGCDNMTMILVQFKKPFAQVKDASD 341
                                                                                                                                                                                       VVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIVQPKQSGVAASSSTD 353
                                        NQFTGIIEGLIWSPKASDSNDRHDD-------WAFEEGPHSDFTGPNCGST
                                                                    AVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVN
             SQLDKLGNG-----NSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarcol R., Gielen J., Van Montagu M., Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C., Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyer A., Weyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO49607; CAB40756.1; -.
EMBL; AL16757; CAB79904.1; -.
EMBL; AY057611; AAL14406.1; -.
HSSP; P35813; 1A6Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                           357
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000222; PP2C.
InterPro; IPR00193; PP2C_domain.
Pfam; PF00481; PP2C; 2.
SMART; SM00332; PP2Cc; 1.
                                                                                                                                                                                                                                                                                           PRELIMINARY;
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STRAIN-CV. COLUMBIA,

WEDLIREA20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo. H., Moffat K.S.,

Croin L.A., Shen M., Vanken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preser S.D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                  HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Cheuk R. Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 CVAVVRDKQLFVANAGDSRCVISRKNQAYNLSRDHKPDLEAEKERILKAGGFIHAGRVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQLDKLGNG-----NSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 VVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAV
                                                                                                                                                                                                                           22;
                                                                                                                                                         Length 357;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 VDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIVQPK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 VDFIHEQLNSETKLSVVCEKVLDRCLAPNTSGGEGCDNMTMILVRFK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
                                                                 98EE1A09818CA0D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHEFICAL 39.4 KDA PROTEIN.
                                                                                                                                                         Score 973; DB 10;
Pred. No. 2e-70;
55; Mismatches 78;
SMART; SM00331; PP2C_SIG; 1. PROSITE; PS01032; PP2C; 1. SEQUENCE 357 AA; 39203 MW;
                                                                                                                                                         53.0%;
55.3%;
                                                                                                                                                         Query Match
Best Local Similarity 55.33
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
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STRAIN-CV. COLUMBIA;
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Query Match
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Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"Full Length cDNA of gene F27C12.1/At2g25070 (GI:4559345).";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006585; AAD33006.1;
EMBL; AX050873; AAK9281001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophia melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGENCE TWO NOTE.

STRAIN-BERRELEY.

MEDLINE-20196006; PubMed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

Wan K. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                                                                                                                                                                                                                                                                              121 SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180
                                                                                                                                                                                                                                                                                                                                                                                                                           119 NKFSGMIEGFIWSPRSGD-----TNNQPDSWPLEDGPHSDFTGPTSGCTACVALI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Gaps
                                                                                                                                                                                                                                                                                                            1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.7%; Score 967; DB 10; Length 355; 53.3%; Pred. No. 6.1e-70; ive 60; Mismatches 93; Indels 1:
                                                                                                                                                                                                                                                                       93; Indels
                                                                                                                                                                                                          CAD638796203C746 CRC64;
                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CG10417 PROTEIN (LD27655P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                              InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
Pfam; PF00481; PP2C; 2.
                                                                                                                                                   SMART; SM00332; PP2Cc; 1.
SMART; SM00331; PP2C_SIG; 1.
PROSITE; PS01032; PP2C; 1.
Hypochetical protein.
SEQUENCE 355 AA; 39354 MW;
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.38
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                   HSSP; P35813;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Rackova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Burtis K.C., Basam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Burtis K.C., Basam D.A., Buller C., Davenport L.B., Davies P., And Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., R., Fosler C., Gabrielian A.E., Garg N.S., Gluan P., Harris M., Harrey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M. H., Ibegwam C., Alalali M., Kalush F., Karpen G.H., Krayitz S., Kulp D., Lai Z., Liang Y., Lin X., Alalali M., Kalush F., Karpen G.H., McZ., Morris J., Moshrefi A., Lasko P., Lei Y., Leitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., Mcried M.P., McPherson D.L., Mortku B., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Stopeler F., Shen H., Rabander K., Saunders R.D.C., Scheeler F., Shen H., Rabine B.C., Siden Krämos I., Simpson M., Strong R., Sun E., Spradling A.C., Stapler B., Weinskern D.R., Weissenbach J., Rabine B.C., Stapletton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Yang S., Yao Q.A., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra Zheng X.H., Romer E.W., Rubin G.M., Venter J.C., Rabengaster T., Scheng K.F., Zaveri J.S., Zhan M., Zhong W., Zhou X., Zhong W., Zhou X., Zhong W., Zhou X., Zhong X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGRRAAALAAEATUKAVMDPSAKPDGSSTSAAAAAAALSADGVANSRNPSNVVNPMAGAD 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawpe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Chorallez M., Guarin H., Li P., Liao G., Miranda A., Mungail C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003787; AAK57333.1; --
EMBL; AR031748; AAK93172.1; --
HSSP; P35813; 1A60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EMMKGASGWKELQSLEETSS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
Pfam; PF00481; PP2C; 2.
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FlyBase; FBgn0033021; CG10417.
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SMART; SM00331; PP2C_SIG; 1.
PROSITE; PS01032; PP2C; 1.
SEQUENCE 662 Aa; 72369 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Y, CN BW SP;
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SEQUENCE FROM N.A.

RADINE-20196006; PubMed=10731132;

REDINE-20196006; PubMed=10731132;

REDINE-20196006; PubMed=10731132;

RADINE-20196006; PubMed=10781132;

RADINE-20196006; PubMed=10791132;

RADINE-20196006; Radine-2019606; Radine-2019606; PubMed=1079; PumMed=1079; PumMe
                                                                                                                                                                                                                359 EDGNEDSDEEETDEDQMANDNFCANMIEEPGKDSGCTAVVCLLQGRDLYVANAGDSRCVI 418
                                                                                                                                                                                                                                                                                                          DKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVKSRLPTTKTLSSLCEEI 316
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                       GPIYGSTAVVALIRGNKLFVANAGDSRCIM
                                                                                                                                                                                                                                                                                  SRRGEAVNLSIDHKPNLEHERKRIESAGGFVH-GGRVNGSLNLTRAIGDMEFKGRPDLPP
                                            239 SNTTTSINDLSTKNAALKDDSVNDQNEGSNGTDFKHTLVSSSNKKLFATGSNDMTELNQS
                                                                                                                                      SKNEFTNSSTSKEFERNINSSQDDEFTDDDADYEENDNVKSPDTSSAESSDCTENDDDGD
-SDYSYAVLTESNDSNLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 LDYCLSPTTR-QQEGCDNMSIIIVQPK-----QSGVAASSSTD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                        159 KKHKY----SDFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2195(2000).
EMBL: AE003477; AAF47746.1; -.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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MEDILINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 -----LRNKTCGDQ------MAGSTAVVVLV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 KDNKLYCANAGDSRAIACVNGQLEVLSLDHKPNNEAESKRIIQGGGWVEFNRVNGNLALS
                                                                                                                                                                                                                                                                                                                                                                              30.4%; Score 558.5; DB 5; Length 371; 37.6%; Pred. No. 5.8e-37;
                                                                                                                                                                                                                                                                                                                          E45A512772C2E36D CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                   50; Mismatches 103;
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                                                                                                                                                                                   FlyBase; FBG00035425; CG17746.
InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C.domain.
Pfam; PF00481; PP2C; 1.
SNART; SM00331; PP2Cc; 1.
SNART; SM00331; PP2C_SIG; 1.
PROSITE; PS01032; PP2C; 1.
                                                                                                                                                                                                                                                                                                                          41009 MW;
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.6
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                        SEQUENCE
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Rablew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beason K.Y., Bernan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Bortier P., Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Bortier P., Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I., Ra Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., A cabibos B., Dalcher A., Dangs Z., Mays A.D., Dew I., Dietz S.M., Ra Durbin K.J., Evangelista C.C., Ferraz C., Evriera B.C., Dunn P., Burtin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K., Andrews D., Heiman T.J., Hermandez J.R., Houck J., Harris N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J., Harris N.L., Andreiel B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., R. Milmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin X., R. Milmel B.E., McIncosh T.C., McLeod M.P., McPherson D.L., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Naktol B., McIncosh T.C., Morris J., Pollard J., Puri V., Reese M.G., R. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shie B.C., Sident-Klamos I., Simpson M., Stupski M.P., Smith T., Shie B.C., Siden E., Spradling A.C., Stapleton M., Stupski M., Wang A.H., Wang S., Yao Q.A., Walbers R.A., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A., R. Hilliams S.M., Woodage T., Wolley K.C., Wang A.H., Wang S., Yao Q., Zhan X., The genome sequence of Drosophila melanogaster."; Smith H.O., R. Hilliams S.M., Moorage T., Wolley C., Staple S., Zhu X., Zhu X., Smith H.O., R. Hilliams S. A., Waper S.W., Rubin G. M., Chuley J.C., Staple S., Stale S., Smith S., Steiner S., Stei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 IRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 SSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 TA------GCTAIVVL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGQTLSEPVTTKDTACCANASYRVGSSCMQGWRVDMEDAHTHILSLPDDPQAAFFAVYDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 TRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38529 MW; D0D1A7CD7D6F53EC CRC64;
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37.2%; Pred. No. 1.6e-36;
Live 47; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
Pfam; PF00481; PP2C; 1.
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SMART; SM00331; PP2C_SIG; 1.
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Best Local Similarity 37.2%
Matches 127; Conservative
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SEQUENCE 352 AA; 38
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            δλ
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REDINING_2019606; Pubbmed=10731132;
RADALN=EARRELEY:
RADARRELEY:
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                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41214 MW; 14380A505621A173 CRC64;
                                                                                Last sequence update)
Last annotation update)
                     367 AA.
                                                           Created)
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SMO0332; PP2Cc; 1.
SMART; SMO0331; PP2Cc_SIG; 1.
PROSITE; PS01032; PP2C; 1.
SEQUENCE 367 AA; 41214 MW;
                                                         (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 126; Conserv
                                                                                                                  CG6036 PROTEIN.
                                                       01-MAY-2000 (
01-MAY-2000 (
01-OCT-2001 (
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                                        Q9VBF9;
                 Q9VBF9
                                                                                                                                        CG6036
Q9VBF9
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1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNV-DKNTSTSIFGIFD 59

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PRT;
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MEDLINE=20196006; PubMed=10731132;
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InterPro; IPR001932; PP2C_domain.
Pfam; PF00481; PP2C; 1.
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SMART; SM00331; PP2C_SIG; 1.
PROSITE; PS01032; PP2C; 1.
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                         Q9VAK1
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                                                                                            Db
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                                                                                                                                                                                                         180 IRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNL 239
                                                                                                                                                                                                                                120 SSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVAL 179
                                                                                                                                                               240 TRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFV 299
                                                                                                                                                                                                                                                                                                        183 SRAFGDYDFKNDGSKSPVDQWVSPEPDIIVCNRSEHDEFIVVACDGIWDVMISSEVCEFI 242
                                                                                                                                                                                                                                                                                                                                                                                     121 SQLDKLGNGNSSSNAREDDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NG-SSGRSRFDDYS-----ADPNDLSES------GCTSNVILI 139
                                                        60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEET 119
                                                                                                                                                                                                                                                                                                                                                               300 KSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPK--QSGVAASSSTD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGNKLFVANAGDSR----CIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSL 237
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Villatobo E., Moch.
A Villatobo E., Moch.
A Villatobo E., Moch.
C., Perasso R., Baroin-Tourancheau A.;
A Villatobo E., Moch.
Thistriomacorum (Ciliophora, Oxytrichidae): a mRNA differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sterkiella histriomuscorum.
Bukaryota; Alveolata; Cillophora; hypotrichs; Stichotrichida;
Oxytrichidae: Sterkiella.
NCBL_Tax1D=94289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.7%; Score 545; DB 5; Length 280;
41.3%; Pred. No. 4.8e-36;
ive 45; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8e-36;
ches 87; Indels
                                                                            280 AA; 31289 MW; 07252EE8D154CA82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 124; Conservative
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RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Barton G.G., Wortman J.R., Yandell M.D., Zhang O., Chan L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazef R.G., Change M., Miklos G.L.G.,
RA Abril J.F., Appayani A., An H.-J., Andrews-Fennkch C., Baldwin D.,
Ballew R.M., Basu A., Barcandale J., Bayrekarsoglu L., Beasley E.M.,
Ballew R.M., Basu A., Barden B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Buchan D.A., Buller H., Cadteu E., Center A., Chandra I.,
Ra Borkova D., Bulcher A., Danck J., Bow I., Dietz S.M.,
Ra Borkova D., Bulcher A., Danck J., Brokstein P., Brottier P., Bortier P.
RA Geris B., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M.,
Roborn R., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Garley B., Delcher A., Moller M. R., Barnis M.,
RA Harris M.L., Harvey D., Haman T.J., Hernandez J.R., Rottok J.,
RA Harris M.L., Harvey D., Haman T.J., Hernandez J.R., Rottok J.,
RA Harris M.L., Harvey D., Haman T.J., Hernandez J.R., Rottok J.,
RA Harris M.L., Harvey D., Haman T.J., Hernandez J.R., Rottok J.,
RA Harris M.L., Maykan R., Moller M., Ralush F., Katpen G.H., Ke Z., Kenitson J.A., Retchum K.A.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McRherson D.L.
Rabon D.R., Moly M. Wurphy B., Murphy L., Murany D.M., Nelson D.L.
Rabon D.R., Moly M. Murphy B., Murphy L., Murany D.M., Nelson D.K.,
Rabon D.R., Moly M. R.A., Nixon K., Nussern D.R., Parley S., Pan S., Pollard J., Moly R., Palazolo M., Pittuma G.S., Pan S., Pollard J., Weissenbach J.,
Rabor P., Lei Y., Wassarman D.A., Weissenbach J.,
Rabor R., Wassarman D.A., Weinster E., Wang G., Yu Wang S., Yu Wang Z., Yu Wassarman D.A., Weissenbach J.,
Rabon R.R., Wassarman D.A., Weissenbach J.,
Rabon R.R., Mayer B.W., Woodege T., Woode K., Weissenbach J.,
Rabon R.R., Wassarman D.A., Weiner E., Wang G., Weissen R.,
Rabon R.R., Rabon R.R.
                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
CG1906.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                238 NLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVD
                                                                                                                                                                                                                                                                                                                         368 AA.
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60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD------LKASLEYSFLRMDEMMKGA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 ----GSTAVGVWVSPTHMYFINCGDSRAVLCRNGQVCFSTQDHKPCNPVEKERIQNAGGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seroussi E., Shani N., Hayut A., Faier S., Ben-Meir D., Divinski I., Smorodinsky N.I., Lavi S.,
"Procedinsky N.I., Lavi S.;
"Protein phosphatase 1B. Cloning and characterization of two major transcripts generated by alternative use of 3' exons.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ1833; CAC28024.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNL
                                                                                 240 TRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFV
                                                                                                                                                                             1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD
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                                                                                                                                                                                                                                               300 KSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV-----QPKQSGVAA 348
                                                                                                                                                                                                                                                                           Length 477;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN PHOSPHATASE 1B2 53 KDA ISOFORM.
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                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    477
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InterPro; IPR001932; PP2C_domain.
Pfam; PP00481; PP2C; 1.
SWART; SM00332; PP2Cc; 1.
SWART; SM00331; PP2C_SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52111 MW;
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01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SEQUENCE 477 AA; 521
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SEQUENCE FROM N.A.
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       TRESEKCG-
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                                                                                                                                                                                                                                                                 GHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEET 119
                                                                                                                                                                                                                                                                                                                                                               SSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 IRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVAL 179
                                                                                                                                                                                                                                                                                             || | | |:: ||||| ::: :| : || : || GHAGCKVSEHCAKHLLESIISTEEFIGGDHVKGIRTGFLRIDEVMR--------ELPEF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ptertygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEET 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GITAVCAF 127
                                                                                                                                                                                              Gaps
                                                                                                                                                                  1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNV-DKNTSTSIFGIFD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNV-DKNTSTSIFGIFD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-Y, CN BW SP;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.

Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (AGG-2001) to the EMBL/GenBank/DbBJ databases.

EMBL; AY051685; AAK93109.1;

SEQUENCE 374 AA; 41629 MW; 37CA399271627F7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 HSRMRVTSNLVSIANQVVDTCLHKGSR-----DNMSIIIIAFPGAPKPTEEAIEA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _
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                                                                            Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 KSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV-----QPKQSGVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                          Indels
     6ED4A4354159F274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.4%; Score 540.5; DB 5; 34.6%; Pred. No. 1.7e-35;
                                                                    29.4%; Score 540.5; DB 5; 34.6%; Pred. No. 1.6e-35; ive 63; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
  40955 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 34.69
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           : : | |
TRESEKCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
     AA;
                                                                                           Local Similarity
nes 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LD23542P.
  SEQUENCE
                                                                         Query Match
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                                                                                                                  Matches
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SECURISE E., Shani N., Hayut A., Faler S., Ben-Meir D., Divinski I.,
A Smorodinsky N.I., Lavi S.;
Trottein phosphatase IB. Cloning and characterization of two major
Transcripts generated by alternative use of 3' exons.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
IS Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
R RBL; AJ271834; CAC28066.1;
R HSSP; P35813; 1A60.
R Interpro; IPR001932; PP2C.
R Interpro; IPR001932; PP2C.domain.
R Pfam; PR00481; PP2C; 1.
R SMART; SM0331; PP2C.5; 1.
R SMART; SM0331; PP2C.5; 1.
R PROSITE; PS01032; PP2C; 1.
O SEQUENCE 465 AA; 51010 MW; A94DB476C48FC136 CRC64;
                                                                                                                                                                           288 DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV~---QPKQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
                                                                                                                                                                                                                                                                    228 VHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD------LKASLEYSFLRMDEMMKGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 VHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                                                                                168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN PHOSPHATASE 1B2 53 KDA ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 534; DB 11;
; Pred. No. 7.6e-35;
54; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 AA.
                                                                121 S-------DLRNGMDRS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 S-----DLRNGMDRS-----
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Thu Jun 20 13:15:30 2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Micoloro S.M.C., Buxton J.M., Bose A., Emoto M.,
Waters S.B., Czech M.P.;

"Potentiation of Insulin Receptor Signaling by Protein Phosphatase
DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KKH-----GADRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQSGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.3%; Score 519; DB 11; Length 3 ilarity 33.9%; Pred. No. 7.3e-34; Conservative 59; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2C.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; APE29673; AAG44662.1;
InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
Fr00481; PP00481; PP2C_1.
SMART; SM00332; PP2C_5: 1.
SMART; SM00331; PP2C_5: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35888 MW; 83B6EF793AE816B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Crea 01-MAR-2001 (TREMBLrel. 16, Last 01-DEC-2001 (TREMBLrel. 19, Last PROTEIN PHOSPHATASE 2C ALPHA 1B.
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01032; PP2C; SEQUENCE 323 AA; 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                      344 SGVA 347
                                                                                                                                                                                                                                                          SDEA 305
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Matches 124;
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Best Local
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09E0E2
AC 09E0E2;
DT 01-MAR-1
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-3
DT
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60 GHGGKLVAKFCAKHLHQEVLKSE-----AYAKGDLKASLEYSFLRMDEMMKGASGWKE 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------KKH-----GADRSG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 SQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQSGVA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                                                                                                                                                             SEQUENCE FROM N.A.
Cherniack A.D., incoloro S.M.C., Buxton J.M., Bose A., Emoto M.,
Waters S.B., Czech M.P.;
"Potentiation of Insulin Receptor Signaling by Protein Phosphatase
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVMS
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EMBL; AF259672; AAG44661.1; -.
HSSP; P55813; 1A60.
InterPro; IPR00022; PP2C.
InterPro; IPR001932; PP2C_domain.
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SMART; SW00332; PP2Cc; 1.
SMART; SW00331; PP2Cc; 1.
SMART; SW00331; PP2Cc; 1.
SEQUENCE 326 AA; 36110 MW; 19AA1994931A823B CRC64;
                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN PHOSPHATASE 2C ALPHA 3.
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Best Local Similarity 33.9%; Pred. No. 7.4e-34;
Matches 124; Conservative 59; Mismatches 111;
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                             PRELIMINARY;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Q99267 mus musculu O88484 rattus norv O88483 rattus norv P35816 bos taurus Q01631 neurospora Q9p011 homo sapien Q01513 podospora a Q9p29 homo sapien P46014 arabidopsis P14605 schizosacch Q15750 homo sapien Q15750 homo sapien	S	STANDARD; PRT; 546 AA. 1. 36, Created) 1. 36, Last sequence update) 1. 40, Last annotation update) tase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma) tase angnesium dependent 1 gamma) (Protein phosphatase	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	le; bMed=9276438; .J.; protein phosphatase with a unique acidic 19(1997).	N 12) TISSUE=Placenta; A Strausberg R: A Strausberg R: C SUDMILLED (NOV-2000) to the EMBL/GenBank/DDBJ databases. C -! - CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE GTHIS ENIZWE IS SERINE/HREONINE SPECIFIC). C -! - COFACTOR: BINDS 2 MAGNESIUM OR MANGARESE IONS (BY SIMILARITY). C -! - SUBCELLUIAR LOCATION: CYtoplasmic (Potential). C -! - SUBCETAL MUSCLE, AND HEART. C -! - SIMILARITY: BELONGS TO THE PP2C FAMILY.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	ne family. (BY SIMILARITY).
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235 6 222.5 7 223.5 7 218.5 9 217.5 0 205.5 1 203.5 1 172 1 158		RESULT 1 P2CG_HUMAN ID P2CG_HUMAN STANDAR AC 015355; DT 15-JUL-1998 (Rel. 36, DT 15-JUL-1998 (Rel. 36, DT 16-OCT-2001 (Rel. 40, DT 16-OCT-2001 (Rel. 40, DE Protein phosphatase 2C DE (Protein phosphatase A	lC). PPMIG OR PPN HOMO Sapiens Eukaryota; M Mammalia; Eu	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=Skeletal muscle; MEDLINE=97420453; PubMed=9276438; Travis S.M., Welsh M.J.; "PPCC gamma: a human protein phospi domain.";	SEQUENCE FRG IISSUE=Place SETAISBEGT F SUBMITTED (N. 1. CATALYTI) ORTHOPH ORTHOPH I COFACTOR I SUBCELLL SUBCELLL SEEEFAAR SKELETAR SKELETAR	This SWISS-PROT entry is copyright. between the Swiss Institute of Biother burpean Bloinformatics Institutes by non-profit institutions a prodified and this statement is not entities requires a license agreement send an email to license@isb-sib.	EMBL; Y13936; CAA74445.1; EMBL; BC000057; AAH00057.1; HSSP; P35813; 1A60. MIM; 605119; InterPro; IPR001922; PP2C. InterPro; IPR001932; PP2C_dom Pfam; PF00481; PP2C_SIG; 1. SMART; SM00331; PP2C_SIG; 1. PROSITE; PS01032; PP2C; 1. Hydrolase; Magnesium; Mangane METAL 40 40
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MEDDIINE-97415625; Pubmed-9271424;
Guthridge M.A., Bellosta P., Tavoloni N., Basilico C.;
FINI3, a novel growth factor-inducible serine-threonine phosphatase which can inhibit cell cycle progression.";
                                                                                                                                                              1 MGIYLCSPKTDKTSEDDENA---ELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGI 57
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Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)
(Protein phosphatase magnesium-dependent 1 gamma) (Protein phosp
IC) (Pibroblast growth factor inducible protein 13) (FIN13).
Mus musculus (Mouse)
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MANGANESE 2 (BY SIMILARITY).
ASP/GLU-RICH ACIDIC.
                                                                                                          35.0%; Score 643; DB 1; Length 546; 32.7%; Pred. No. 2.4e-42; Live 60; Mismatches 112; Indels 168;
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MGD; MGI:106065; Ppmlg.
InterPro: IPR000222; PP2C_domain.
InterPro: IPR001932; PP2C_domain.
Pfam; PF00481; PP2C; 2.
SMART; SM0031; PP2C_SIG; 1.
SMART; SM0032; PP2CC; 1.
Hydrolase; Magnesium; Manganese; Multigene family; Nuclear protein;
SEQUENCE OF 123-420 FROM N.A.

SEQUENCE OF 123-420 FROM N.A.

Guthridge M.A., Seldin M., Basilico C.;

Induction of expression of growth-related genes by FGF-4 in mouse
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; Pred. No. 3.1e-42;
63; Mismatches 111; Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASP/GLU-RICH (ACIDIC).
EDED -> NSAR (IN REF. 2).
1DC72E7A66E71453 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE PP2C FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U42383; AAC26322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.9%;
                                                                                                                        Oncogene 12:1267-1278(1996)
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438
493
319
126
58728 1
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161; Conservative
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438
493
258
123
542 AA;
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10;

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                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein phosphatase 2C gamma isoform (BC 3.1.3.16) (PP2C-gamma)
(Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase
1B) (Magnesium-dependent calcium inhibitable phosphatase) (MCPP).
     203
                                                                                 263 CCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVKSRLP-----TTKTLSSLCEEI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i - CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)0 = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
-i - COPACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
-i - SUBCELLULAR LOCATION: CYCOPIASMIC (Potential).
-i - SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                  SYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEA
                                                             204 VNLSIDHKPNLEHERKRIESAGGFV-HGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANGANESE 1 (BY SIMÎLARITY).
MANGANESE 1 (BY SIMÎLARITY).
MANGANESE 1 AND 2 (BY SIMÎLARITY).
MANGANESE 2 (BY SIMÎLARITY).
MANGANESE 2 (BY SIMÎLARITY).
ASP/GLU-RICH ACIDIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huang C.Y., Qin K.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD1898195E234A94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000222; PP2C.
InterPro; IPR000322; PP2C.
InterPro; IPR001931; PP2C.
SMART; SM00331; PP2C.SIG; 1.
SMART; SM00332; PP2Cc; 1.
PR0STITE; PS01032; PP2Cc; 1.
Hydrolase; Magneslum; Manganese; Multigene family.
                                                                                                                                                                                                                                                                                                        543 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU
                                                                                                                                                                                       LDYCLSP-TTRQQEGCDNMSIIIV 339
                                                                                                                                                                                                                        LDQCLAPDTSGDGTGCDNMTCIII 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U81159; AAB39357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
439
494
258
266
306
543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                    P2CG_BOVIN
P79126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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 144
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Length 543;

Score 641; DB 1; Pred. No. 3.4e-42;

34.9%; 32.0%;

Best Local Similarity

Query Match

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298
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                                                                                                                                                                                                                                                                                                                                                                                                                                          FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSL- 116
                                                                                                                                                            ----EETSSQLDKL------GNG 129
                                                                                                                                                                                                                                                         179 EEPGSQGLNGEAGPEDPSRETSAEVNGPTAKAHTGLSSNSECGTEAGQGGEPGTPTGEAG 238
                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                        204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 CPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVKSRLP-----TTKTLSSLCEEIL 317
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wedler H., Wambutt R., Lyne M., Rajandream M.A., Barrell B.G.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
TRANSMITTED THROUGH WIS1 MAP KINASE.
-!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + ORTHOPHOSPHATE (THIS ENZIME IS SERINE/THREONINE SPECIFIC).
-!- CATALYTICS AND SUBME AND STABLES IN SECURIOR (BY SIMILARITY).
-!- COFACTOR: BINDO 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
                                                   MGIYLCSPKTDKTSEDDENAE---LRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGI 57
                                                                                                                                                                                                                                                                                          ------EDDESDYSYAVLTESNDSNLATKKHKYSDFQ-----
                                                                                                                                                                                         119 GRPTEDEDEKEKVADEDDVDNEEAALLHEEATMTIEELLTRYGQNCHKGAPHSKSGAGTG
                                                                                                                                                                                                                                                                                                                                                        -------GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAV
                                                                                                                                                                                                                                                                                                                                                                         299 EEAEEDDEEEEMWYPGMEGKEEPGSDSGTTAVVALIRGKQLIVANAGDSRCVVSEAGKAL
                                                                                                                                                                                                                                                                                                                       239 PSCSSASDKLPRVDKSKFFEDSEDESDEAEEEEEDSEECSEEEDGYSSEEAENEEDEDDT
                                                                                                                                                                                                                                                                                                                                                                                                                      NLSIDHKPNLEHERKRIESAGGFV-HGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PP2C) and a MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fission yeast.";
 166;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
PTC2 OR SPCC1223.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae;
 Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shiozaki K., Russell P.;
"Counteractive roles of protein phosphatase 2C
Minase kinase homolog in the osmoregulation of
EMBO J. 14:492-502(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYCLSP-TTRQQEGCDNMSIIIVQPKQSGVAA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ||:| |: || DOCLAPDTSGDGTGCDNMTCIIICFKPRNTAA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972;
MEDLINE=95163582; PubMed=7859738;
 64;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896
                                                                                                                                                          117 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P2C2_SCHPO
Q09172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=972;
 Matches 164;
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                                                                                            28
                                                                                                                                                                                                                          130
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, Hanke C.,
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Q09173;
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SEQUENCE
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METAL
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                               116 LEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 IFDGHGGKLVAKFCAKHLHQEVLKSE-AYAKGDLKASLEYSFLRMDEMMKGASGWKELQS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DMQEDPSGCTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQA 294
                                                                                                                                                                                                                                                                                                                                                                    1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILN-VDKNTS---TSIFG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVALIRGNK-LFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                           Manganese; Multigene family.

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                            34.6%; Score 635; DB 1; Length 370; 41.6%; Pred. No. 5.9e-42; Live 48; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 VVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQ-QEGCDNMSIIIV 339
                                                                                                                                                                                                                                                                             DBDDB826F440AC50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Portein phosphatase 2C (EC 3.1.3.16) (PP2C).
Paramecium tetraurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 AA
SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                   EMBL; AL031579; CAA20880.1; -...
HSSP; P35813; 1A60.
InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C.
Pfam; PF00481; PP2C; 1.
SMART; SM00331; PP2C_SIG; 1.
SMART; SM00332; PP2Cc; 1.
Hydrolase; Magnesium; Manganese; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=51S;
MEDLINE-95105156; PubMed=7806499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                             40878 MW:
                                                                                                           EMBL; L34881; AAA67320.1;
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                 38
63
233
282
                                                                                                                                                                                                                                           63
233
282
370 AA;
                                                                                                                                                                                                                                                                                                                       Local Similarity
es 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P2C_PARTE
P49444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paramecium
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                              Query Match
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METAL
METAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GCTANVALI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
             MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
BC0318B4FF7724EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 616.5; DB 1; Length 300;
; Pred. No. 1.2e-40;
61; Mismatches 99; Indels 51
Donella-Deana A., Beyer A., Kellner R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STIGGAQVTEELLKKAAEDLLDQLLAPDTSQGTGCDNMTTILV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRL----PITKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV 339
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(Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DTDESYA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P35813; 1A6Q.
InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
Pfam; PF00481; PP2C; 1.
SMART; SM00331; PP2C_SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01032; PP2C; 1.
Hydrolase; Magnesium; Manganese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.68;
38.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z36985; CAA85448.1; -. HSSP; P35813; 1A6Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
33739 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 38.55
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                    Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.

-! FNUOTION: HAS AN IMPORTANY ROLE IN OSMOTIC STABILITY AND CELL
SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
-! CAPALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
-! COFRACTOR: BINDS: A MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 ETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------FHTDPSGCTATV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGQILSEPVTEKHSVNGSNEFVLYGLSSMQGWRISMEDAHSAILSMECSAVKDPVDFFAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNT---STSIFGI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiozaki K., Russell P.; "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase homolog in the osmoregulation of fission yeast."; EMBO J. 14:492-502(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MANGANESE 1 (BY SIMÍLARITY).
MANGANESE 1 (BY SIMÍLARITY).
MANGANESE 1 (BY SIMÍLARITY).
MANGANESE 2 (BY SIMÍLARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
01-NOV-1997 (Rel. 35, Last annotation update)
Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
PTC3 OR SPAC2G11.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> T (IN REF. 1).
EFF3A416625A2B11 CRC64;
                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00331; PP2C_SIG; 1.
SMART; SM00332; PP2Cc; 1.
PR0STIE; PS01032; PP2C; 1.
Hydrolase; Magnesium; Manganese; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.18; Score 608.5; DB 1; 40.2%; Pred. No. 7.5e-40; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
                                                                                                                                                                                 MEDLINE=95163582; PubMed=7859738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L34882; AAA67321.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z54354; CAA91172.1; -. P35813; 1A6Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00481; PP2C; 1.
                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                      297
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
-!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
178 ALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSL
                NLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Magnesium; Manganese.

1 MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
16-0C7-2001 (Rel. 40, Last sequence update)
16-0C7-2001 (Rel. 40, Last annotation update)
Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.0%; Score 606; DB 1; Length 356; 37.0%; Pred. No. 9.8e-40; tive 58; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             (OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                             298 FVKSRLPTTKTLSSLCEEILDYCL-SPTTRQQEGCDNMSIIIV 339
                                                                                                                                Æ.
                                                                                                                                                                                                                 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Sim
hes 131;
                                                                                                                                                                                                               P2C2_CAEEL
P49596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durbin R.;
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                 Swinburne
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS
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METAL
SEQUENCE
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Matches
                                                                                                                                                                                    RESULT 7
P2C2_CAEEL
                                                                                                                                         244
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us-09-828-302-14.rsp

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                                                                                                                                                                                                        241 RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK 300
HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                    ------KDDVSGTTAVVVLI 124
                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditída; Rhabditoldea;
Rhabditídae; Peloderinae; Caenorhabditís.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taich A., Waterston R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H (2)O = A PROTEIN +
- OFTHOPHOSPHATE (THIS ENZYME IS SERINE/THERONINE SPECIFIC).
-!- COFACTOR: BINDS 2 MAGNESIUW OR MANGANESE IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                          121 SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI
                                                                                                                                       RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT
                  Hydrolase; Magnesium; Manganese.

MANGANESE I (BY SIMILARITY).

MANGANESE I (BY SIMILARITY).

MANGANESE I AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                            SRLPTTKTLSSLCEEILDYCLSPTTRQQE-GCDNMSIIIVQPKQSGVAASSSTD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-6C7-1996 (Rel. 34, Last sequence update)
01-80V-1997 (Rel. 35, Last annotation update)
Probable protein phosphatase 2C F42G9.1 (EC 3.1.3.16) (PP2C).
                                                                                                                                                                                                                                                                                                                                                                                                     491 AA
                                                                                                    WormPep; F42G9.1; CE07231.

InterPro; IPR000222; PP2C.

InterPro; IPR001932; PP2C_domain.

PEdm; PF00481; PP2C; 2.

SMART; SM00331; PP2C_SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U00051; AAA91358.1; -. HSSP; P35813; 1A6Q.
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                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 P2C1_CAEEL
P49595;
01-FEB-1996 (
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SEQUENCE
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DB 1; Length 491;

555.5; DB 1 No. 1.2e-35;

Score Pred.

58;

30.

Similarity

Query Match Best Local 9

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SEQUENCE FROM N.A.

CARAIN-S288C / AB972;

CARAIN-S288C / ABAGRESION OR ABAGANESE DONS (BY SIMILARITY)
                                                                                                                                                                              HGGTEVSKFTSAKLPDFLKERKFWEADDVAECLQKAFVDFDDFIRAEESMKELKDIGDEG 118
                                                                                                                                                                                                                                                                                                                                                                  419 EDEFIVVACDGIWNSMESQOVVDFVRDLLAKGSSCAEVCDALCDACLADSTDGDGTGCDN 478
                                                                                              HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQ----- 114
                                                                                                                                                            -----------SLEETSSOLDK------LGNGNSSSNARE 137
                                                                                                                                                                                                                                                     179 EDEDEEEAEEODDTEEKKENEDASAEVVIENAEDKEEEEGSPKKKGOKRCOKSPIOSEAK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 GDEFIVLACDGIWDVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTT-RQQEGCDN 333
                                                    1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                         215 EHERKRIESAGGFVHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGP
                                                                                                                                                                                                                                                                                                                                                 ------FQGPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
   Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Maeda T., Tsai A.Y.M., Saito H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     ----ESDYSYAVLTESNDSNLATKKHKYSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AA.
   Mismatches
65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                        138 DD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 MSII 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTVI 482
 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P2C2_YEAST
P39966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P2C2_YEAST
   Matches
                                                                                              61
                                                                                                                                                          115
                                                                                                                                                                                                                                                                                     140
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 EETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 VALI -- RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVMSSQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 AVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQE-GCDNMSIIIVQPKQSGVAASSST 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNV----DKNTSTSIFG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 40, Last annotation update)
Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
(Protein phosphatase IB).
PPMIB OR PPPMIB OR PP2C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                            MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
61D82D2CA4ED3FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                    30.2%; Score 554.5; DB 1; Length 436.8%; Pred. No. 1.3e-35; .ive 50; Mismatches 113; Indels
                                                                                                                                                                                                               SMART; SM00331; PP2C_SIG; 1.
SMART; SM00332; PP2Cc; 1.
PR0STTF; PS01032; PP2Cc; 1.
Hydrolase; Magnesium; Manganese; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 AA.
                                                                                                       EMBL; U18839; AAB64644.1; --
EMBL; U72489; AAB17392.1; --
HSSP; P35813; 1A60.
SGD; S0000891; PTC2.
InterPro; IPR000222; PP2C.
InterPro; IPR0001932; PP2C_domain.
Pfam; PF00481; PP2C; 1.
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                                                                                                                                                                                                                                                                                                                                                       50388 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                      464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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P36993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
Yanagawa Y., Katsura K., Hiraga A., Tamura S.;

Alternative promoters direct tissue-specific expression of the mouse
protein phosphatase 2cbeta gene.";

Eur. J. Biochem. 263:736-745(1999).

C. - FUNCTION: BUXZME WHITH A BROAD SPECIFICITY.

- TOTALYICA ACTIVITY: A BROAD SPECIFICITY.

- TOTALYICA ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).

- COFACTOR: BINDS 2 MACHESIUM OR MANGANESE IONS (BY SIMILARITY).

- COFACTOR: BINDS 2 MACHESIUM OR MANGANESE IONS (BY SIMILARITY).

- ALTERNATIVE PRODUCTS: 5 ISOFORMS; BETA-1 (SHOWN HERE), BETA-2,
BETA-3, BETA-4 AND BETA-5; ARE PRODUCED BY ALTERNATIVE SPLICING.

- ALTERNATIVE PRODUCTS: 5 ISOFORMS; BETA-1 IS EXPRESSED EXCLUSIVELY IN THEIR C-TERMINUS.

- TISSUE SPECIFICITY: BETA-1 IS EXPRESSED UBIQUITOUSLY; BETA-2 IS
EXPRESSED EXCLUSIVELY IN BRAIN AND INTESTINE.

- SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                             MEDLINE-95251388; PubMed=7733667;
Kato S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.;
Molecular cloning and expression of mouse Mg(2+)-dependent protein
phosphatase beta-4 (type 2C beta-4).";
Arch. Blochem. Blophys. 318:387-393(1995).
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
MEDLINE=94313028; PubMed=8038726;
MEDLINE=94313028; T., Miyasaka H., Li S.S.;
Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
"Molecular cloning and expression of cDNAs encoding two isoforms of protein phosphatase 2C beta from mouse testis.";
Biochem. Mol. Biol. Int. 32:773-780(1994).
                                                                               Tanaka O., Kondo H., Yamamoto H., Takeuchi T., Tamura S.;
Molecular cloning of a novel isotype of Mg(2+) dependent protein
phosphatase beta (type 2C beta) enriched in brain and heart.";
Arch. Biochem. Biophys. 307:342-349(1993).
                  SEQUENCE FROM N.A.
MEDLINE-94099616; PubMed-8274020;
Terasawa T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
                                                                                                                                                                                        SEQUENCE FROM N.A. (BETA-3; BETA-4 AND BETA-5).
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMEL; AB007796; BAA84471.1; JOINED. PRE, AB007797; BAA84471.1; JOINED. PIR; S39780; S39780. HSSP; P35813; 1A60. MGD; MGI:101841; Ppm1b. InterPro: IPR000222; PP2C. InterPro: IPR001932; PP2C_domain. Pfam; PF00481; PP2C; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB007798; BAA84471.1; -. AB007794; BAA84471.1; JOINED. AB007795; BAA84471.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/SV;
MEDLINE=99398339; PubMed=10469137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D45861; BAA08295.1; -. U09218; AAB60442.1; -.
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SDEAVKKDSE 311
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                                                                                                                                      GAGDLEDSLVAL -> MADLSTSICKPS (IN ISOFORM BETA-4).
                                                                                                                                                                                                                                                                                                  108 SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
GAGDLEDSLVAL -> VSLHIFFRKIK (IN ISOFORM
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                          VAL -> FYQPSIAYSDNVFLL (IN ISOFORM BETA-
                                                                                                                                                                                                                                                            1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDELINE-98348020; PubMed-9684878;
Marely A.E., Kline A., Crabtree G., Sullivan J.E., Beri R.K.;
"The cloning expression and tissue distribution of human PP2Cbeta.";
                                                                                                                                                                                                                                                                                                                                                                   168 GPIYGGTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF
                                                                                                                                                                                                                                                                                                                                                                                                         VHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIW
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta)
PPMIB OR PP2CB.
                                                                                                          BETA-2).
GAGDLEDSLVAL -> FYQPSIAYSDNVFLL
                                                                                                                                                                                                         29.4%; Score 539; DB 1; Length 390; 33.5%; Pred. No. 1.7e-34;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                             255C97B4276189FD CRC64;
                            Hydrolase; Magnesium; Manganese; Multigene family;
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                                                                                                                              ISOFORM BETA-3)
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                                                                                                                                                                                                                             58; Mismatches
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SMART; SM00331; PP2C_SIG; 1.
         SMART; SM00332; PP2CC; 1.
PROSITE; PS01032; PP2C; 1.
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                                                                                                                                                                                                                             Conservative
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60
243
286
390
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                                       Alternative splicing.
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                                                                                                                                                                            390 AA;
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286
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Matches 124;
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075688;
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                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND SKELETAL MUSCLE. SIMILARITY: BELONGS TO THE PP2C FAMILY.
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-:- CATALYTICA ACTUITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
-:- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
-:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS SUCH AS BETA-X (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER IN THEIR C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GHGGKLVAKFCAKHLHQEVLKSEAY-AKGDLKASLEYS------FLRMDEMMKGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF 227
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MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
A345797ADZ63DFBD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%; Score 538; DB 1; Length 479; 34.6%; Pred. No. 2.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001222; PP2C.
InterPro; IPR001932; PP2C_domain.
Pfam; PF00481; PP2C. 1.
SMART; SM00331; PP2C_SIG; 1.
SMORT; SM00332; PP2Cc; 1.
PROSITE; PS01032; PP2C; 1.
Alternative splicing.
MANGANESE 1 (BY SIMILA
METAL.
37 MANGANESE 1 (BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S------SLRNGMDRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ005801; CAA06704.1; -. HSSP; P35813; 1A6Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 M
52642 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
243
286
279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVAASSSTD 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
                                                                                                                                                                                                                                                                                         Klumpp S., Selke, D., Fischer D., Baumann A., Mueller F., Thanos S., "Profein phosphatase type-2C isozymes present in vertebrate retinae: purification, characterization, and localization in photoreceptors."; J. Neurosci. Res. 51:328-338(1998).
-!- FUNCTION: ENZYME WITH A BRADAD SPECIFICITY.
-!- FUNCTION: ENZYME WITH A BRADAD SPECIFICITY.
-!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
-!- COPACION: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
-!- SUBBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GSTAVGVMISPKHIYFINCGDSRAVLYRSGQVCFSTQDHKPCNPREKERIQNAGGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHGGKLVAKFCAKHLHQEVLKSEAY-AKGDLKASLEYS------FLRMDEMMKGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANGANESE 1 (BY SIMÍLARITY).
MANGANESE 1 (BY SIMÍLARITY).
MANGANESE 1 AND 2 (BY SIMÍLARITY).
MANGANESE 2 (BY SIMÍLARITY).
D70B95141250FFB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.2%; Score 537; DB 1; Length 38'34.9%; Pred. No. 2.4e-34;
Live 56; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Magnesium; Manganese; Multigene family.
   387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DLRNGMDRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C_domain.
                                                                                                                                                                                                                                                                          MEDLINE=98146173; PubMed=9486768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ005458; CAA06555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00481; PP2C; 1.
SMART; SM00331; PP2C_SIG; 1.
SMART; SM00332; PP2Cc; 1.
PROSITE; PS01032; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                   Bovidae; Bovinae; Bos
                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P35813; 1A60.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                              rissue-Retina;
P2CB_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILNE-94205266; PubMed-8154187; Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.; "Sequencing and functional analysis of a 32,560 bp segment on the left arm of yeast chromosome II. Identification of 26 open reading frames, including the KIPl and SEC17 genes."; Yeast 9:1355-1371(1993).
                    DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ 343
                                                                                    228 VHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maeda T., Wurlger-Murphy S.M., Saito H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
ORTHOPHOSPHAFE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
-!- COFFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Manganese; Multigene family. | Manganese; Multigene family. | 37 | Manganese | (BY SIMILARITY). | 38 | Manganese | (BY SIMILARITY). | 52 | MANGANESE | (BY SIMILARITY). | 534 | MANGANESE | (BY SIMILARITY). | 569 | D -> G (IN REF. 2). | 51390 | MW; | DC5C18053828DC0D | CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                     P34221; 092330;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
PTC3 OR YBL056W OR YBL0511 OR YBL0513.
                                                                                                                                                                                                                                                            468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, 223261, CAA80791.1; -.
EMBL, 235817; CAA84876.1; -.
EMBL, 072346, AAB1351.1; -.
PIR, 53982. S3983.
PIR, 537333; 537333.
HSSP, P35813; IAGO.
SGD, S0000152; PTC3.
InterPro; IPR000222; PPC2.
InterPro; IPR000222; PPC2.
                                                                                                                                                                                                                                                            PRT;
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SMART; SM0031; PP2C_SIG; 1.
SMART; SM0031; PP2C_SIG; 1.
PROSITE; PS01032; PP2C; 1.
Hydrolase; Magnesium; Manganess
METAL 37 37 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369
51390 D
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                    344 SGVAASSSTD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
369
468 AA;
                                                                                                                                                                     302 SDEAMRKDSE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C
                                                                                                                                                                                                                                                          P2C3_YEAST
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                      P2C3_YEAST
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Biochem, Biophys. Res. Commun. 207:708-714(1995).

-I - FUNCTION: ENZYME WITH A BROAD SPECIFICITY.

-I - CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)0 = A PROTEIN +
ORTHOPHOSPHOPTE (FINE ENZYME IS SERINE/THREONINE SPECIFIC).

-I - COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).

-I - SUBUNIT: MONOMER (BY SIMILARITY).

-I - ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS SUCH AS BETA-1 (SHOWN HERE) AND BETA-MPP ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER IN THEIR C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                          FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMD-EMMKGASGWKELQSL 116
                                                                                                                                                                                           EETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAV 176
                                                                                                                                                                                                                            ------GCTAT 123
                                                                                                                                                                                                                                                         177 VALIRGNK -- LFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVN 234
                                                                                                                                                                                                                                                                           GSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVMSSQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schafer K., Braun T.; "Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wenk J., Trompeter H.-I., Pettrich K.-G., Cohen P.T.W., Campbell D.G.
                                                                1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAH---KAILNVDKNTSTSIFGI 57
                                                                                   Mieskes G.; "Molecular cloning and primary structure of a protein phosphatase 2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P35815; Q64046;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
                                                                                                                                                  |||||| ||:|| : | |::| |::|
FDGHGGSSVAEFCGSKMISTLKKQESFKSGMLEQCLIDTFLATDVELLKD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                  :99
 DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                       294 AVVDEVKSRLPT-TKTLSSLCEEILDYCLSPTTRQQE-GCDNMSIIIV 339
                                                                                                                                                                                                                                                                                                                                                                                                      244 ECVDLVHYGISQGNMTLSDISSRIVDVCCSPTTEGSGIGCDNMSISIV 291
                              109; Indels
29.2%; Score 537; DB 1
38.8%; Pred. No. 3e-34;
                              38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                 -----EKT--------EKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM BETA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;
MEDLINE-92201367; PubMed=1312947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
MEDLINE~95169115; PubMed-7532404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBS Lett. 297:135-138(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Protein phosphatase 1B).
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                              Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P2CB_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .soform.
                  Best Local
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                                                                                                                                                                                           117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
GAGDLEDSLVAL -> FYQPSTPYSDNVSYYEWQT (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 S.----- DLRNGMDRS----- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ----GSTAVGVMISPTHIYFINGGDSRAVLCRNGQVCFSTQDHKPCNPMEKERIQNAGGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 VHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-------LKASLEYSFLRMDEMMKGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 DVMSNEELCEFVNSRLEVSDDLENVCNWVVDTCLHKGSR-----DNMSIVLVCFANAPKV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
PPMIA OR PPPMIA OR PP2C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%; Score 534; DB 1; Length 390; 34.3%; Pred. No. 4.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D147615BC2FA140B CRC64;
                                                                                                                                                                                              InterPro: IPR00022; pp2C.
InterPro: IPR01932; pp2C_domain.
InterPro: IPR00332; pp2C_domain.
SMART: SM00331; pp2C_sIG; 1.
SMART: SM00332; pp2Cc; 1.
PR0STIPE: PS01032; pp2Cc; 1.
Hydrolase; Magnesium; Manganese; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOFORM BETA-MPP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MM;
                                                                                                                        EMBL; S90449; AAB21898.1; -. EMBL; S74572; AAB33430.1; -. PIR; S20392; S20392. HSSP; P35813; 1A60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                            Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P2CA_RAT
P20650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 RVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVM 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 SSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQSGV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 ELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 GSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GHGGKLVAKFCAKHLHQEVLKSEAYAKG------DLKASLEYSFLRMDEMMKGASGWK 111
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                              MANGANESE 1 (BY SIMÍLARITY).
MANGANESE 1 (BY SIMÍLARITY).
MANGANESE 1 AND 2 (BY SIMÍLARITY).
MANGANESE 2 (BY SIMÍLARITY).
MANGANESE 2 (BY SIMÍLARITY).
CIC386E935374F89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.4%; Score 522; DB 1; Length 382; Best Local Similarity 34.1%; Pred. No. 3.3e-33; Matches 125; Conservative 59; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manganese; Multigene family.
                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A32399; A32399.
HSSP; P35813.1A60.
InterPro; IPR00022; PP2C.
InterPro; IPR001932; PP2C.
InterPro; IPR001932; PP2C.
SMART; SM00481; PP2C, 11.
SMART; SM00331; PP2C, 11.
PROSITE; PS01032; PP2C, 11.
PROSITE; PS01032; PP2C, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J04503; AAA41917.1; -.
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                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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METAL
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| :
| Db | 301 AVKKEAE 307
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Search completed: June 19, 2002, 08:47:49 Job time: 223 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:42:46; Search time 20.94 Seconds (without alignments)
1619.844 Million cell updates/sec
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Title: US-09-828-302-14
Perfect score: 1836
Sequence: 1 MGIYLCSPKTDKTSEDDENA......MSIIIVQPKQSGVAASSSTD 353
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283138 Minimum DR see length. 0

283138 segs, 96089334 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution,

	Description	protein phosphatas		hosphata		protein phosphatas		hypothetical prote			•~		_		phosphoprotein pho			2	phosphoprotein pho	hypothetical prote	protein phosphatas	probable protein p		probable protein p	doudsoud	Et.			hosphata	phosphoprotein pho
SUMMARIES	QI	T06308	H84643	S54297	A55804	S62462	E88434	T25181	T16354	S50592	S65672	~~	539832	S20392	JC2524	A32399	S22422	153823	S22423	T21331	T08853	E84748	T45778	F84650	S48288	B86209	T50783	F84695	F96752	c
	DB	7	~	7	~																									
	Length	357	355	370	300	414	348	356	491	464	390	393	468	390	397	382	382	382	382	468	920	380	361	392	393	442	348	362	511	359
dФ	Query	53.0	52.7		33.6					30.2	29.4		29.3	29.1	29.1	28.4				27.5										19.3
	Score	973	196	m	616.5	608.5	909		555.5	വ	539	539	537	534	534	522	520	519	517	505.5	457	415.5	403.5	401.5	398.5	363.5	358	357	355	354.5
	Result No.	Н	7	Э	4	2	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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RESULT

phosphoprotein pho	probable protein p	protein phosphatas	phosphoprotein pho	hypothetical prote	phosphoprotein pho	phosphoprotein pho	phosphoprotein pho	hypothetical prote	hypothetical prote	protein phosphatas	phosphoprotein pho	protein F12A21.5 [protein phosphatas	protein phosphatas	probable protein p
T04263	T02483	C85323	T09019	T05095	A56058	S41854	S55457	F86206	T48018	T09640	A47492	н96700	T08606	C84826	T00750
7	a	N	~	~	~	~	7	~	~	~	~	N	7	7	7
434	386	388	386	389	347	281	399	405	383	381	406	464	975	390	404
19.3	19.3	19.1	18.9	18.9	18.7	18.6	18.2	18.0	17.8	17.8	17.8	17.7	17.7	17.2	17.1
					Ŋ	5	334	30	327	۲.	326	25	.5	۲.	14
	353.5	350.5	346.5	346.	343.	341.	'n	S.	æ	326.5	m	m	324	315	314

ALIGNMENTS

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RESULT 1 T06308 C;Species: 30- C;Species: 30- C;Accession R;Bevan, H.W.; ewes,	RESULT 1 To6308 Tortein phosphatase 2C homolog F11C18.60 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001 C:Accession: T06308 R:Bevan, M.: Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, 1 ewes, H.W.; Mayer, K.F.X.; Schueller, C. Submitted to the Protein Sequence Database, April 1999 A;Reference number: 215589 A;Accession: T06308 A;Accession: T06308 A;Residues: 1-357 < EBC>	A;Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:FI1C18.60 A;Experimental source: cultivar Columbia; BAC clone F11C18 C;Genetics: A;Gene: ATSP:FI1C18.60 A;Map position: 4 A; Map position: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3 C;Superfamily: human phosphoprotein phosphatase 1A	Query Match 53.0%; Score 973; DB 2; Length 357; Best Local Similarity 55.3%; Pred. No. 1.2e-70; Matches 192; Conservative 55; Mismatches 78; Indels 22; Gaps 3;	1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60	HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEVSFLRMDEMMKGASGWKELQSLEETS 120 	SQLDKLGNGNSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTA 175 :::	VVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNG 235 :: : CVAVVRDKQLFVANAGDSRCVISRKNQAYNLSRDHKPDLEAEKERILKAGGFIHAGRVNG 223	SLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIMDVMSSQAV 295 :	VDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIVQPK 342 :
REGULT T06308 T06308 Totein C.Species C.Species R.Bewes, H. A.Rebidit A.Resida A.Recene: A.Resida A.Re	phoses: Page 18 30-Page 18 30-Pag	refe iment ics: ATSE Ositi ns: 3	Matc Local es 1	1 MC			76 VA 1 64 CV		
	SULT 6308 otein Specil Date: Acces, H bmitt Refer Refer Moleci	Cross Cross Gene: Gene: Map p. Intro	Query Best Match						
	PP TO CO.	र व र व व व व र		QY DP	Qy Dp	Qy Db	QY	Qy	Qy Db

Gaps

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A,Cross-references: EMBL:AL031579; PIDN:CAA20880.1; GSPDB:GN00068; SPDB:SPCC1223.11
A,Experimental source: strain 972h-; cosmid c1223
C,Genetics: SPCC123.11
A,Gene: SPCC1223.11
A,Map position: 3
C;Superfamily: human phosphoprotein phosphatase 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 LEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGFIYGSTA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFDGHGGKLVAKFCAKHLHQEVLKSE-AYAKGDLKASLEYSFLRMDEMMKGASGWKELQS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....NALMQDR-----DMQEDPSGCTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 VVALIRGNK-LFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- 133
                                                                                                                                                                                                                                                                                                                                                                             1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILN-VDKNTS---TSIFG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                  Length 370;
                                                                                                                                                                                                                                                                                      90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 VVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQ-QEGCDNMSIIIV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.6%; Score 616.5; DB 2; 38.5%; Pred. No. 4.7e-42;
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                                                                                                                                                                                                                               34.6%; Score 635; DB 2;
41.6%; Pred. No. 2.1e-43;
iive 48; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                          Best Local Similarity 41.6%
Matches 144; Conservative
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Matches 132;
                                                                                                                                                                                                                               Query Match
Best Local 3
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                                                                                                                                              C.Y.;
lon, L.
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            probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Decies: Arabidopsis thaliana (mouse-ear cress)
C:Accession: H84643
R:Lin, X: Kaul, S: Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Jatitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Accession: H84643
A;Accession: H846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein phosphatase 2C homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: S54297; T40871
R;Shiozaki, K.; Russell, P.
BMBO J. 14, 492-502, 1995
A;Tills: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase la, Reference number: S54297; MUID:95163582
A;Reference number: S54297
A;Accession: S54297
A;Accession: S54297
A;Molecule type: DNA
A;Residues: 1-370 <SHI>A;Residues: 1-370 <SHI>A;Residues: 1-370 <SHI>A;Counteractive number: Special kinase kinase la, Residues: 1-370 <SHI>A;Residues: 1-370 <SHI>A;Residues: 1-370 <SHI>A;Residues: 1-370 <SHI>A;Counteractive number: September 1998
B;Bounted to the EMBL Data Library, September 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| :| | ::| | ::| | | ::| | EQLKSETKLSTVCEKVVDRCLAPDTATGEGCDNMTIILVQFKKPNPSETEPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.7%; Score 967; DB 2; Best Local Similarity 53.3%; Pred. No. 3.5e-70; Matches 188; Conservative 60; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-370 <WED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: At2g25070
A;Map position: 2
C;Superfamily: human phosphoprotein phosphatase
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Accession: T40871
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protein T23F11.1 [imported] - Caenorhabditis elegans
C;Species; Caenorhabditis elegans
C;Species; Caenorhabditis elegans
C;Species; Caenorhabditis elegans
C;Species; Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C;Accession: B88434
R;anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:chr_III; PIDN:CAA86456.1; PID:g3880103; GSPDB:GN00021; CESP:T2
C;Genetics:
A;Gene: T23F1.1
A;Map position: 3
C;Superfamily: human phosphoprotein phosphatase 1A
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 24-Aug-2001
C;Accession: T25I81
R;Swinburne, J.
R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGP1YGSTAVVALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 3
A;Introns: 35/1; 132/1; 207/1; 255/3; 280/3; 308/3; 332/1
C;Superfamily: human phosphoprotein phosphatase 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.0%; Score 606; DB 2; L
37.0%; Pred. No. 4.1e-41;
Live 58; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RVDEET----
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Best Local Simi
Matches 131;
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-414 GAB2-3
A.Cross-references: EMBL:254354; NID:g1019398; PIDN:CAA91172.1; PID:g1019405; GSPDB:GNOG
A.Experimental source: strain 972h-; cosmid c2G11
A.Statosaki, K.; Russell, P.
EMBO J. 14, 492-502, 1995
A.Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase hc
A.Reference number: S54297; MUID:95163582
A.Accession: S54298
A.Status: preliminary
A.Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein phosphatase 2c homolog 3 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001 C2Accession: T38573; S54285
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995
      240
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A;Cross-references: EMBL:L34882; NID:g609657; PIDN:AAA67321.1; PID:g609658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLE 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVD 297
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                                RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT
                                                                                                                         RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
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                                                                                                                                                                                                                                                                                | STIGQAQVTEELLKKAAEDLLDQLLAPDTSQCTGCDNWTTLV 296
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40.2%; Pred. No. 3.3e-41;
tive 48; Mismatches 96;
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A;Introns: 110/1; 134/3
C;Superfamily: human phosphoprotein phosphatase lA
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Matches 138; Conservative
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A; Accession: T38573
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hypothetical protein YER089c - yeast (Saccharomyces cerevisiae)

(Species: Saccharomyces cerevisiae

(Species: Saccharomyces cerevisiae

(Species: Saccharomyces cerevisiae

(Spacession: S50592

Schare: 28-Way-1993 #sequence_revision 24-Feb-1995 #text_change 15-Jun-2001

(Spacession: S50592

Submitted to the EMBL Data Library, December 1994

A; Description: The sequence of S. cerevisiae cosmids 9747, 8198, 9781, and lambda clo

A; Reference number: S50436

A; Molecule type: DNA

A; Molecule type: DNA

A; Molecule type: DNA

A; Cross-references: EMBL:U18839; NID:g603313; PIDN:AAB64644.1; PID:g603327; MIPS:YER0

C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 AVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQE-GCDNMSIIIVQPKQSGVAASSST 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .-----GCTAT 123
                                                                                                                                                                                   | |:|| | |: || || || APLLLGSGGAEVPGEDSGTTACVCLVGKDXVIVANAGDSRAVLCRNGKAVDLSVDHKPED
                                                                                                                                 1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNV----DKNTSTSIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 VALI -- RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 DCVDLVHLGLREGKTLNEISSRIIDVCCAPTTEGTGIGCDNMSIVVVALLKEGEDVAQWS
KSKSETDAETAPSSSGVDGVATEEEDEDDSDKEFVADEEEDDEDAEDEQSDEEMVDGSL
                                   -----FQGPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNL
                                                                                                           EHERKRIESAGGFVHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVMSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.2%; Score 554.5; DB 2; ilarity 36.8%; Pred. No. 8.6e-37; Conservative 50; Mismatches 113;
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A;Cross-references: SGD:S0000891; MIPS:YER089c
A;Map position: 5R
C;Superfamily: human phosphoprotein phosphatase
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MTVI 482
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Best Local Simi
Matches 133;
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239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F42G9.1 - Caenorhabditis elegans
C; Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T16354
A; Praich, A.
Submitted to the EMBL Data Library, March 1996
A; Reference number: 218498
A; Reference number: 218498
A; Reference number: 116354
A; Accession: T16354
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-491 C/AI>
A; Cross-references: EMBL: U00051; NID: 91216305; PID: 91216310; PIDN: AAA91358.1; CESP: F42G9
C; Genetics: C; Genetics: A; 364/2; 364/2; 364/2; A06/2
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                                                                                                                                                                                                                                           SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180
                                                                                                                                                                                                                                                                                                                   181 RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT 240
                                                                                                                                                                                                                                                                                                                                                                                             RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HGGSKVSQYSGINLHKKVVAQKEFSEGNMKEAIEKGFLELDQQM------- 104
                                                                                                                                                                                                                                                                               HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQ----- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----------SLEETSSQLDK-------LGNGNSSSNARE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDEDEEEAEEQDDTEEKKENEDASAEVVIENAEDKEEEEGSPKKKGQKRCOKSPIOSEAK 238
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                               1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRLPTTKTLSSLCEEILDYCLSPTTRQQE-GCDNMSIIIVQPKQSGVAASSSTD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 491;
               Length 356;
             33.0%; Score 606; DB 2; Length 35 37.0%; Pred. No. 4.2e-41; ive 58; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 555.5; DB 2;
; Pred. No. 7.7e-37;
65; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ESDYSYAVLTESNDSNLATKKHKYSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.3%;
Best Local Similarity 28.5%;
Matches 138; Conservative 69
                                                     Conservative
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD-----
                                                   Matches 131;
             Query Match
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A;Cross-references: EMBL:D45859; NID:g961469; PIDN:BAA08293.1; PID:g961470
A;Experimental source: tissue testis:
R;Terasawa, T.; Kobayashi, T.; Murakami, T.; Ohnishi, M.; Kato, S.; Tanaka, O.; Kondo Arch. Biochem. Biophys. 307, 342-349, 1993
A;Title: Molecular cloning of a novel isotype of Mg(2+)-dependent protein phosphatase A;Teterence number: S39780; MUID:94099616
A;Accession: S39780
                                                                                                                                                                                                                                                                                                                A; Accession: 39760
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Accession: 393781
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-378, VSLHIFPKYLK' <TE2>
A; Residues: 1-378, VSLHIFPKYLK' <TE2>
C; Genetics: CB:D17412; NID:9452527; PIDN:BAA04234.1; PID:d1004753; PID:945252
C; Genetics: CB:D17412; NID:9452527; PIDN:BAA04234.1; PID:d1004753; PID:945252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: PP2C
C;Superfamily: human phosphoprotein phosphatase 1A
C;Keywords: magnesium; phosphoric monoester hydrolase; serine/threonine-specific phos
F;37,38,60/Binding site: magnesium 1 (Glu, Asp, Asp) #status predicted
F;60,243,286/Binding site: magnesium 2 (Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHGGKLVAKFCAKHLHQEVLKSEAYAKGD------LKASLEYSFLRMDEMMKGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGWRVEMEDAHTAVVGIPHGLDNWSFFAVYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF
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33.5%; Pred. No. 1.2e-35;
Live 58; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-----DLRNGMDRS-----
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Best Local Similarity 33.5%
Matches 124; Conservative
A; Molecule type: mRNA
A; Residues: 236-393 <KAT>
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N.Alternate names: phosphoprotein phosphatase lA beta-3
C.Species: Mus musculus (house mouse)
C.Species: Musculus (house mouse)
C.Species: Musculus (house mouse)
C.Species: Mayasaka, H.; Li, S.S.
Biochem. Mol. Biol. Int. 32, 773-780, 1994
A.Ritle: Molecular cloning and expression of CDNAs encoding two isoforms of protein phos A.Reference number: 149016
A.Restaus: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-393 <-RES
A.Residues: 1-393 <-RES
A.Residues: 1-393 <-RES
A.Cross-references: EMBL.009218; NID:9484099; PIDN:AAB60442.1; PID:9484100
A.Raperimental source: tissue testis
R.Kato, S.; Terasawa, T.; Kobayashi, T.; Ohnishi, M.; Sasahara, Y.; Kusuda, K.; Yanagawa Arch. Biochem. Bio
                       phosphoprotein phosphatase (EC 3.1.3.16) lA-beta-4 - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28. Cut. 1996 #sequence_revision l3-Mar-1997 #text_change l5-Jun-2001
C;Accession: S65672
R;Kato, S.; Terasawa, T.; Kobayashi, T.; Ohnishi, M.; Sasahara, Y.; Kusuda, K.; Yanagawa Arthe: Biochem. Biophys. 318, 387-393, 1995
A;Title: Molecular cloning and expression of mouse Mg(2+)-dependent protein phosphatase A;Reference number: S65670; MUID:95251388
A;Accession: S65672
A;Accession: S6572
A
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C;Superfamily: human phosphoprotein phosphatase 1A
C;Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHGGKLVAKFCAKHLHQEVLKSEAYAKGD------LKASLEYSFLRMDEMMKGA 107
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Matches 124; Conservative
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phosphoprotein phosphatase (EC 3.1.3.16) lA-beta - rat
NyAlternate names: magnesium-dependent protein phosphatase lA; protein serine/threoni
C;Species: Rattus norvegicus (Norway rat)
C;Accession: JC2524
E;Schaefer, K.; Braun, T.
Biochem: Biophys. Res. Commun. 207, 708-714, 1995
A;Title: Monoclonal anti-flag antibodies react with a new isoform of rat Mg2+ depende
A;Reference number: JC2524; MUID:95169115
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A; Residues: 1-397 <SCH>
A; Cross-references: GB:S74572; NID:g807067; PIDN:AAB33430.1; PID:g807068
A; Experimental source: brain
C; Superfamily: human phosphoprotein phosphatase 1A
C; Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase
F; 206-213/Region: FLAG peptide
                                                                                                                                                                                                                                                    DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ 343
                                                                                                                                            SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
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54; Mismatches
                                                            60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD~
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Matches 125; Conserva
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N.Alternate names: protein phosphatase 2C.2
C.Specias: Rattus norvegicus (Norway rat)
C.Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 15-Jun-2001
C.Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 15-Jun-2001
C.Accession: S20392
R.Wenk, J.; Trompeter, H.I.; Pettrich, K.G.; Cohen, P.T.W.; Campbell, D.G.; Mieskes, (FEBS Lett. 297, 135-138, 1992
A.Title: Molecular cloning and primary structure of a protein phosphatase 2C isoform. A.Reference number: S20392; MUID:92201367
A.Status: not compared with conceptual translation
A.Molecule type: MRNA
A.Residues: 1-390 <MRNA
A.Residues: 1-390 <MRNA
A.Residues: 1-390 <MRNA
        A; Cross-references: EMBL:223261; NID:9313733; PIDN:CAA80791.1; PID:9313742
A; Experimental source: strain S288C
R; Dubols, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, submitted to the Protein Sequence Database, August 1994
A; Reference number: 845782
A; Accession: S45791
                                                                                                                                       A;Cross-references: GB:S90449; NID:9247926; PIDN:AAB21898.1; PID:9247927
C;Superfamily: human phosphoprotein phosphatase 1A
C;Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMD-EMMKGASGWKELQSL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FDGHGGSSVAEFCGSKMISILKKQESFKSGMLEQCLIDTFLATDVELLKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        109;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.2%; Score 537; DB 2; Best Local Similarity 38.8%; Pred. No. 2.2e-35; Matches 135; Conservative 38; Mismatches 109
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phosphoprotein phosphatase (EC 3.1.3.16) lA - rat
N.Alternate names: protein phosphatase 2C
Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A32399
R;Tamura, S.; Lynch, K.R.; Larner, J.; Fox, J.; Yasul, A.; Kikuchi, K.; Suzuki, Y.; Tsui
Proc. Natl. Acad. Sci. U.S.A. 86, 1796-1800, 1989
A;Title: Molecular cloning of rat type 2C (IA) protein phosphatase mRNA.
A;Reference number: A32399; MUID:89184515
A;Accession: A32399
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-382 < TAM.
A;Residues: 1-382 < TAM.
A;Cross-references: GB:J04503; NID:9206312; PIDN:AAA41917.1; PID:9206313
C;Superfamily: human phosphoprotein phosphatase lA
C;Keywords: liver; phosphoric monoester hydrolase; serine/threonine-specific phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 GNEELCDFVRSRLEVTDDLEKVCNEVVDTCLYKGSR-----DNMSVILICFPNAPKVSAE 300
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288 DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ 343
                       60 GHGGKLVAKFCAKHLHQEVLKSEAYAKG------DLKASLEYSFLRMDEMMKGASGWK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIY 171
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Best Local Similarity 34.1%; Pred. No. 2.7e-34;
Matches 125; Conservative 59; Mismatches 109; Indels
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Sequence 4,

Sequence 2, Al Sequence 2, Al Sequence 4, Al Sequence 2, Al Sequence 2, Al Sequence 2, Al Sequence 54, Al Sequence 6, Al Sequence 14, Al Seque

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35.0%; Score 643; DB 3; Length 546; 32.7%; Pred. No. 9.3e-61; Live 60; Mismatches 112; Indels 1
                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08935855
Patent No. 6066485
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER FOLDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JGCKSON ESQ:, David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 201-343-1684
US-08-530-198-4
US-08-656-880-4
US-08-728-70-4
US-08-719-641-4
US-09-308-375-2
US-09-308-375-2
US-08-125-077-4
US-08-131-131-14
US-08-131-14-14
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 32.77
Matches 165; Conservative
    TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-935-855-20
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Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
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Sequence 8, Appli
Sequence 9, Appli
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Sequence 22, Appl
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                                                                                                                                                  US-09-828-302-14
1836
1 MGIYLCSPKTDKTSEDDENA......MSIIIVQPKQSGVAASSSTD 353
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-935-855-20
US-08-873-093-1
US-08-873-093-1
US-08-873-093-1
US-08-822-701-7
US-08-935-855-7
US-08-935-855-2
US-08-935-855-2
US-08-935-855-2
US-08-935-855-2
US-08-935-855-2
US-08-935-855-2
US-08-935-855-2
US-08-935-855-10
US-08-9406-854-6
                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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US-08-949-941B-2
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Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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1 MGIYLCSPKTDKTSEDDENA---ELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGI 57
                  ------EDDESDYSYAVLTESNDSNLATKKHKYSDFQ------
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
GITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08935855
Patent No. 6066485
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Clauddio
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE,
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION THUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201-343-1684
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07601
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179 DEPGPQGLNGEAGPEDPSRETPSQENGPTAKGHTGFSSNSEHGTEAGQISEPGTATGEAG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GRPTEDEDDKDKVADEDDVDNEEAALLHEEATMTIEELLTRYGQNCQKVPPHTKSGIGTG 178
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                       1 MGIYLCSPKTDKTSEDDENA - - - ELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 SYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEA
                                                                                                                                                                                                                                                                               Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                     58 FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMM-------
                                                                                                                                                                                                                                       34.9%; Score 641.5; DB 3; Length 542; 31.9%; Pred. No. 1.3e-60; ive 63; Mismatches 111; Indels 169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KGASGWK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08B73093;
Patent No. 5853997;
CANERAL INFORMATION:
CAPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Preeti
APPLICANT: Zhang, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 LDQCLAPDTSGDGTGCDNMTCIII 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 LDYCLSP-TTRQQEGCDNMSIIIV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3174 Porter Drive
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
                                 TYPE: amino acru
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                       ; ORGANISM: Mus musculus US-08-935-855-22
                                                                                                                                                                                                                                         Query Match 34.9
Best Local Similarity 31.9
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palo Alto
                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-873-093-1
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60 GHGGKLVAKFCAKHLHQEVLKSEAY-AKGDLKASLEYS------FLRMDEMMKGA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GSTAVGVMISPKHIYFINGGDSRAVLYRNGQVCFSTQDHKPCNPREKERIQNAGGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 VHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQOEGCDNMSIIIV----QPKQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 DVMSNEELCEYVKSRLEVSDDLENVCNWVVDTCLHKGSR-----DNMSIVLVCFSNAPKV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 S------DLRNGMDRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.3%; Score 538; DB 2; Length 470
Best Local Similarity 34.6%; Pred. No. 1.7e-49;
Matches 128; Conservative 57; Mismatches 109; Indels
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0319 US
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION UNDBER: 36,749
REFERENCE/DOCKET MUMBER: PF-03
TELECOMMUNICATION INFORMATION:
TELEFRAN: 415-85-0555
TELEFRAN: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LIBRARY: GenBank
; CLONE: 1452526
US-08-873-093-4
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                                                                                                                         USA
                                                                                                                                          94304
                                                                                                      STATE: CA
                                                                                                                     COUNTRY:
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US-08-873-093-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 DVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 DVMSNEELCEYVKSRLEVSDDLENVCNWVVDTCLHKGSR-----DNMSIVLVCFSNAPKV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GHGGKLVAKFCAKHLHQEVLKSEAY-AKGDLKASLEYS------FLRMDEMMKGA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.3%; Score 538; DB 2; Length 478; 34.6%; Pred. No. 1.7e-49; Live 57; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 S------DLRNGMDRS------
                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ for Windows Version
CURRENT APPLICATION DATA:
PRPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                              APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTCHNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERBENCHOCKTEN NUMBER: PF-0319 US
TELEPANONE: 415-855-0555
ITELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08873093
Patent No. 5853997
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 34.68
Matches 128; Conservative
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: THPIPLB01
CLONE: 13177
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SDEAVKKDSE 311
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60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLE-----YSFLRMDEMMKGAS 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFV 228
247 DVMSNEELCEFVNSRLEVSDDLENVCNWVVDTCLHKGSR-----DNMSIVLVCFANAPKV 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56; Mismatches 104; Indels
                                                                                                                                                                                                                                     APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 533.5; DB 2;
Pred. No. 2.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1049-1-002 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        US-08-822-701-7; Sequence 7, Application US/08822701; Sequence 7. S976853; Patent No. 5976853; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.18;
34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 309 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus US-08-822-701-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 34.77
Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: SIGNODOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                         344 SGVA 347
                                                                             302 SDEA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GSTAVGVMISPIHIYFINCGDSRAVLCRNGQVCFSTQDHKPCNPMEKERIQNAGGS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LKASLEYSFLRMDEMMKGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.1%; Score 534; DB 2; Length 390; 34.3%; Pred. No. 3.3e-49; Live 54; Mismatches 109; Indels
                                                                         APPLICANT: GOli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Dang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 S-----DLRNGMDRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
Sequence 3, Application US/08873093 Patent No. 5853997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 390 amino acids
amino acid
                                                            Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1247927
                                                                                                                                                                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                    Patent No. 5853997
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                94304
                                                                                                                                                                                                                    ADDRESSEE:
                                                        APPLICANT:
                                                                                                                                                                                                                                                          CITY: Pa
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sin
Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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og o	VMSNEELCEFVKSRLEVSDDLENVCNWVVDTCLHKGSRDNMSVVLVCFSNAPKVS	7 a	
RESULT	RESULT 7	oy (289 VMSSQAVV
Sequ Pate	708-953-853-7 Patent No. 6066485	gg —	247 VMSNEEI
GE	GENERAL INFORMATION: APPLICANT: Guthridge, Mark	RESULT US-08-	RESULT 8
	5	. Sec	Sequence 8, Appl
., _	IIILE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE TILLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13 NIMBRE OF SECTIONS. 22	GI	GENERAL INFORMA
. •	NORESPONDENCE SUCCESSION OF THE SUCCESSION OF TH		APPLICANT:
	ADDRESSEE: DAVIG A, JACKBOH, ESG. STREET: 411 Hackensack Ave, Continental Plaza, 4th STREET: nload		TITLE OF INVE
	144		CORRESPONDENC
	H E		ADDRESSEE: STREET: 41
J	LIF: U/6UL COMPUTER READABLE FORM:	~ ~	STREET: F1 CITY: Hack
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible		re: NTR3
	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30		ZIP: 07601 COMPUTER READ
_	CURKENT APPLICATION DATA: APPLICATION NUMBER: US/08/935,855		MEDIUM TYE COMPUTER:
	FILING DATE: CLASSIFICATION: 435		OPERATING S SOFTWARE:
. 7	ATTORNEY/AGENT INFORMATION: NAME: Jackson Esg., David A.		CURRENT APPLI
	REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1049-1-002 CIP		FILING DATE
	ION:		ATTORNEY/AGEN
TAIL	0,		REGISTRATIO
Ž			KEFERENCE/D TELECOMMUNICA
			TELEPHONE: TELEFAX:
	STRANDEDNESS: SINGle TOPOLOGY: linear	Fi	INFORMATION FOR SECUENCE CHAR
~ 14	된 :		LENGTH: 30
. ~ (TYPE:		H .
•	ORGANISM: Mus musculus		TOPOLOGY: MOLECULE TYPE
9	1,425-455-1		HYPOTHETICAL: FRAGMENT TYPE
Que	۽ ب		ORIGINAL SOUR
Mat	<pre>LMITATILY 34./%; ; Conservative 56</pre>	30-S0	US-08-822-701-8
Qy Db	1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNIST-SIFGIFD 59	Quer Best Matc	Query Match Best Local Simil Matches 125; C
Qy Dp	60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGAS 108 	ζς, QΩ	1 MGIYLCSP : 1 MGAFLDKP
Οy	109 GWKELQSLEETSSQLDKLGNGNSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQG 168	δδ	₩.
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                             VVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFV 228
                                               AAKECAKHLHQEVLKSEAYAKG------DLKASLEXSFLRMDEMMKGASGWK 111
 129
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Jarity 34.6%; Pred. No. 7.3e-48;
Conservative 58; Mismatches 104; Indels 74; Gaps
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Guthridge, Mark

Guthridge, Mark

Basilico, Claudio
INVENTION: OVEL GROWTH FACTOR INDUCIBLE
INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
SEQUENCES: 18
DENCE ADDRESS:
EE: David A. Jackson, Esq.

411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/NS-DOS
PATENTIN Release #1.0, Version #1.30
LICATION DATA:
ON NUMBER: US/08/822,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATE:
CCATION: 435
GENT INFORMATION:
CCATION: David A.
TION NUMBER: 26,742
TION NUMBER: 1049-1-002 N
IICATION INFORMATION:
E: 201-487-5800
ATE: 201-487-5800
ES: 201-87-1684
FOR SEC ID NO: 8:
-----DLRNGMDRS----
                                                                                                                                                                                                                                                          lication US/08822701
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ino acid
ESS: single
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PE: protein
L: NO
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sw Jersey
USA
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291 SSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQSGV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::|||:||| | ::||:|| | 246 GNEELCDFVRSRLEVTDDLEKVCNEVVDTCLYKGSR-----DNMSVILICFPNAPKVSAE 300
                                                                                                                                            112 ELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIY 171
                                                                                                                                                                                                                                         ------GADRS 125
                                                                                                                                                                                                                                                                                                                                                              232 RVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVM 290
                                                                                                                       GHGGKLVAKFCAKHLHQEVLKSEAYAKG------DLKASLEYSFLRMDEMMKGASGWK 111
                                                                                                                                                                                                                                                                                172 GSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGG 231
                                                                 1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFD 59
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
  58; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-822-701-2; Sequence 2, Application US/08822701; Sequence 2, Application US/08822701; Patent No. 5976653; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
  Matches 125;
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186 RVNGSLAVSRALGDFDYKCVHGKGPTEQLVSPEPEVHDIERSEEDDQFIILACDGIWDVM 245
                                      112 ELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIY 171
                                                                              ------WASE-----KKH-----GADRS 125
                                                                                                                                            RVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVM 290
                                                                                                                                                                                                                                                                              291 SSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV----QPKQSGV 346
                                                                                                                                                                                                                                                                                                       172 GSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGG
61 GHAGSQVAKYCCEHLLDHITNNQDF-KGSAGAPSVENVKNGIRTGFLEIDEHMR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
APPLICANT: Guthridge, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 22
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ADPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 520; DB 3;
Pred. No. 7.3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1049-1-002 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/935,855 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08935855 Patent No. 6066485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.3%;
34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-935-855-8
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us-09-828-302-14.rai

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Indels

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112 ELQSLEETSSQLDKLGNGNSSSNA-REDDESDYSYAVLTESNDSNLATKKHKYSDFQGPI 170
                                                        171 YGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFV-H 229
                                                                                                                                                                      230 GGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDV 289
                                                                                                                                                                                                                                                              290 MSSQAVVDFVKSRLP-----TTKTLSSLCEEILDYCLSP-TTRQQEGCDNMSIIV 339
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPEDIDENCE ADDRESS:
ADDRESSEE: Incvte n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 370.5; DB 4;
Pred. No. 1.6e-31;
 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
   44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0470 US
                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09013881
Patent No. 6132964
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFRENCE/COCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.2%;
28.0%;
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TYPE: amino acid
STRANDEDNESS: single
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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US-09-013-881-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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 Matches 109;
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                                                                                                                                                                                                       171 YGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFV-H 229
                                                                                                                                                                                                                         230 GGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDV 289
                                                                                                                                                                                                                                                                                             112 ELQSLEETSSQLDKLGNGNSSSNA-REDDESDYSYAVLTESNDSNLATKKHKYSDFQGPI 170
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                              290 MSSQAVVDFVKSRLP----TTKTLSSLCEEILDYCLSP-TTRQQEGCDNMSIIIV 339
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                                                                 Length 392;
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/935,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 491.5; DB 3;
Pred. No. 1.3e-44;
                                                                 26.8%; Score 491.5; DB 2; 46.0%; Pred. No. 1.3e-44;
                                                                                                    44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Beq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08935855 Patent No. 6066485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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46.0%;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal
; FRAGMENT TYPE: N-terminal US-08-822-701-2
                                                                                                  Conservative
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NO
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Best Local Similarity
                                                                                  Similarity
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US-08-935-855-2
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                                                                                                  Matches 109;
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Length 392;

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122 QLDKLGNGNSSSNAREDDESDYSYAVL----TESNDSNLATKKHKYSDFQGPIYGSTAV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 LNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVV 296
                                                                                                                                                                                                                                                                             66 VAKFCAKHLH----QEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETSS 121
                                                                                                                                                                                               14 SEDDENAELRYGLSAMQG------WRDSMEDAHKAILNVDKNTSTSIFGIFDGHGGKL 65
                                                                                                                                                                                                                      85;
                                                                                                                  Length 281;
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US-08-93-585-9
US-08-93-585-9
Sequence 9, Application US/08935855
Setent No. 6066485
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 DFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
                                                                                                                                                        52; Mismatches 110;
                                                                                                                Score 341.5; DB 2;
Pred. No. 1.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1049-1-002 CIP
    ; FRAGMENT TYPE:
, ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
US-08-822-701-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/935,85
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: 201-487-5800
                                                                                                                18.6%;
28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: 281 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            Conservative
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CLASSIFICATION: 435
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New Jersey
                                                                                                                  Query Match
Best Local Similarity
Matches 96; Conserv
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  FRAGMENT TYPE:
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12;
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                                                              264 QYEERMRIQKAGGNVRDGRVLGVLEVSRSIGDGQYK-----RCGVTSVPDIRRCQLT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 SLITRVSYFAVFDGHGGIRASKFAAQNLHQNLIRK--FPKGDVISVEKTVKRCLLDTFKH 197
                                                                                                                                                                                             100 MDEMMKGASGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                   274 PGDEFIVLACDGIWDVMSSQAVVDFVKSRLPTTK-----TLSSLCEILDYCL 321
                                       12 KTSEDDEN-----AELRYGL---SAMQGWRDSMEDAHKAILNVDKN---- 49
                                                                                                                  ---TSTSIFGIFDGHGGKLVAKFCAKHLHQEVLKSEAYAKGD------LKASLEYSFLR 99
                                                                                                                                                                                                                                                                                                                                                      214 LEHERKRIESAGGFVHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG
94; Indels 119;
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APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCTBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
                                                                                                                                                                                                                         Mismatches
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REFERENCE/DOCKET NUMBER: 1049-1-002
TELECOMMUNICATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08822701 Patent No. 5976853 GENERAL INFORMATION:
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 SPTTRQQEGCDNMSIIIVQ 340
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
Matches 106; Conservative
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STATE: New Jersey
COUNTRY: USA
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12;

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Length 314; Indels

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121 SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWD-VMSSQAVV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 DFVKSRLPTTKTLSS----LCEEILDYCLSPTTRQQEGCDNMSIIIVQPKQ-SGVAASSS 351
                                                                                                                                                                                                                                                                                                                                                                           61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
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                                                                                                                                                                                                                                                                          120;
                                                                                                                                                                                                                                        17.8%; Score 326; DB 2;
30.2%; Pred. No. 7.2e-27;
iive 48; Mismatches 120
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                                314 amino acids
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.2%
Matches 109; Conservative
                                                   single
linear
E:
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                        Leishmania
                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                      ; ORGANISM:
US-08-822-701-10
                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 286
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                                                                                                                                                                                                                                                                                                                                                                          122 QLDKLGNGNSSSNAREDDESDYSYAVL----TESNDSNLATKKHKYSDFQGPIYGSTAV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 LNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVV 296
                                                                                                                                                                                                                                                                                                        66 VAKFCAKHLH----QEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETSS 121
                                                                                                                                                                                                       Gaps
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Patent No. 5976853
GENERAL INFORMATION: GLATHING MARK
APPLICANT: BASILICO, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SRINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 DFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| ::::::| 246 ELIKDITEPNEAAKVLVRYALE---NGTT-----DNVTVMVV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                18.6%; Score 341.5; DB 3; 28.0%; Pred. No. 1.3e-28; tive 52; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 201-48-5800
TELEFAX: 201-343-1684
                                                                                                ) ORGANISM: Saccharomyces cerevisiae US-08-935-855-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
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STATE: New Jersey
COUNTRY: USA
                linear
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                                             HYPOTHETICAL: NC FRAGMENT TYPE: ORIGINAL SOURCE:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	QI		AAG43887	AAG43888	AAG43238	AAG43889	AAG43239	AAG11786	AAG11785	AAG11784	AAB82980	ABB59430
	DB	21	21	21	21	21	21	21	21	21	22	22
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df	Query Match	53.0	52.7	47.3	47.2	45.6	45.3	41.6	41.6	41.6	36.5	35.7
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ALIGNMENTS

RESULT

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 54019.
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         AAG43237 standard; Protein; 357
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99US-0126785
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25-MAR-1999;
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16-APR-1999;
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Llarity 55.3%; Pred. No. 7.8e-82;
Conservative 55; Mismatches 78; Indels 2:
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                                                                                                                                                                                                                                                                                                              52.7%; Score 967; DB 21; 53.3%; Pred. No. 2.8e-81;
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                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 LKASLEYSFLRMDEMMKGASGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: || :| |||:||:| ||:|| | : :: : | | | | 59 vetslrraffrmddmmggqrgwrelavlgdkmnkfsgmiegfiwsprsgd------ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHKPNLEHERKRIESAGGFVHGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVV 268
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52.0%;
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30-AUG-1999

31-AUG-1999

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\pm 2 \pm 3 \pm 5 \pm 5
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05 - MAR - 1999;

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PR 23-AUG-1999;
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                                                                                                                                              DEFIVIACDGIWDVMSSQAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMS 335
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                 Query Match

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Best Local Similarity 51.6%; Pred. No. 2.3e-69;
Matches 164; Conservative 55; Mismatches 87;
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289 iilvqfkkpnpseteped 306
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cdnmtmilvrfk 295
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990S-0161992.
990S-0161993.
                                                                                                                                99US-0160815
99US-0160980
                                                                                                                                                 99US-0160981
99US-0160989
                                                                                                                     99US-0160814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
13-0CT-1999;

14-0CT-1999;

14-0CT-1999;

14-0CT-1999;

14-0CT-1999;

18-0CT-1999;

18-0CT-1999;

21-0CT-1999;

21-0CT-1999;

21-0CT-1999;

22-0CT-1999;

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28-0CT-1999;
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09 - JUL - 1999; 13 - JUL - 1999; 13 - JUL - 1999; 14 - JUL - 1999; 16 - JUL - 1999; 16 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 20 - JUL - 1999; 21 - JUL - 1999; 21 - JUL - 1999; 21 - JUL - 1999; 21 - JUL - 1999; 22 - JUL - 1999;	23.JUL.1999; 23.JUL.1999; 23.JUL.1999; 27.JUL.1999; 27.JUL.1999; 27.JUL.1999; 27.JUL.1999; 27.JUL.1999; 28.JUL.1999; 02.AUG.1999; 04.AUG.1999; 04.AUG.1999; 05.AUG.1999; 06.AUG.1999; 06.AUG.1999; 06.AUG.1999; 11.AUG.1999; 11.AUG.1999; 11.AUG.1999; 11.AUG.1999; 11.AUG.1999;	16-AuG.1999; 18-AuG.1999; 20-AuG.1999; 20-AuG.1999; 20-AuG.1999; 23-AuG.1999; 23-AuG.1999; 25-AuG.1999; 27-AuG.1999; 27-AuG.1999; 31-Au
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	0/- MAY 11999; 14 - MAY 11999; 14 - MAY 11999; 14 - MAY 11999; 18 - MAY 11999; 18 - MAY 11999; 20 - MAY 11999; 21 - MAY 11999; 22 - MAY 11999; 23 - MAY 11999; 24 - MAY 11999; 26 - MAY 11999; 27 - MAY 11999; 38 - MAY 11999; 39 - MAY 11999; 30 - MAY 11999; 30 - MAY 11999; 30 - MAY 11999; 30 - MAY 11999; 31 - MAY 11999;	, , , , , , , , , , , , , , , , , , ,
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hybridisation assay; genetic mapping; gene expression control; promoter;
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99US-0132048.
99US-0132407.
99US-0132484.
99US-0132485.
99US-0132486.
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990S-0137222
990S-0137228
990S-013724
990S-0138094
990S-0138840
990S-0138840
990S-0139452
990S-0139452
990S-0139452
990S-0139454
990S-0139454
                                                                                                                                        99US-0121825.
99US-0123180.
99US-012548.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0128784.
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990S-0130077.
990S-0130449.
990S-0130510.
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990S-0134256.
990S-0134218.
990S-0134219.
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99US-0134370.
99US-0134768.
99US-0134941.
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990S-0135353.
990S-0135629.
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99us-0136392.
99us-0136782.
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99US-0139460.
99US-0139461.
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                                                                                                                   2000EP-0301439
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                 termination sequence
                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 - JUN - 1999;
18 - JUN - 1999;
                                                                                                                                        25 - FEB - 1999

05 - MAR - 1999

23 - MAR - 1999

25 - MAR - 1999

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21 - JUN - 1999

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23 - MAY - 1999

24 - MAY - 1999

25 - MAY - 1999

26 - JUN - 1999

27 - JUN - 1999
                                                                                                                   25-FEB-2000;
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10-JUN-1999;
10-JUN-1999;
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16 - JUN - 1999;
16 - JUN - 1999;
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18-JUN-1999;
18-JUN-1999;
                                                                                         06-SEP-2000
     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQSLEETS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 SRLPTTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIVQPKQSGVAASSSTD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.6%; Score 764; DB 21; Length 336; 50.9%; Pred. No. 1.8e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 10637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG11784 standard; Protein; 339 AA
                                      990S-0157753.
990S-0157865.
990S-0158029.
990S-0158232.
990S-0158369.
                                                                                                                                                                                                                                                                                                                    990S-0160989
990S-0161404.
990S-0161406.
990S-0161406.
990S-0161359.
  99US-0156458.
99US-0156596.
99US-0157117.
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99US-0161993.
99US-0162142.
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99US-0159330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.9
Matches 149; Conservative
28-SEP-1999,
29-SEP-1999,
06-0CT-1999,
06-0CT-1999,
07-0CT-1999,
13-0CT-1999,
13-0CT-1999,
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28-0CT-1999,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG11784;
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905-0140695 905-0140823 905-0140823 905-0141284 905-0141284 905-014280 905-0142920 905-0142920 905-0143624 905-0143624 905-0144085 905-0144085 905-0144085	99US-0144332. 99US-0144333. 99US-0144333. 99US-0144335. 99US-0144884. 99US-0144884. 99US-0146886. 99US-0145086. 99US-0145087. 99US-0145087. 99US-0145087. 99US-0145087. 99US-0145087. 99US-0145192. 99US-014518. 99US-0145918.	905-0146389 905-0147038 905-0147038 905-0147192 905-0147192 905-0147260 905-0147360 905-0147361 905-0147319 905-0148311 905-0148341 905-0148341 905-0148341 905-0148341	905-0149175 905-0149426 905-0149426 905-0149929 905-0149930 905-0149930 905-0150566 905-0151066 905-0151066 905-0151066 905-0151066 905-0151080 905-0151080
4 JUN -1999 9 -UN -1999 9 -UN -1999 0 -UN -1999 1 -UL -1999 6 -UL -1999 6 -UL -1999 6 -UL -1999 7 -UL -1999 6 -UL -1999	19-70L 1999; 19-70L 1999; 19-70L 1999; 20-70L 1999; 20-70L 1999; 21-70L 1999; 22-70L 1999; 22-70L 1999; 22-70L 1999; 22-70L 1999; 23-70L 1999;	2 - AUG - 1999 3 - AUG - 1999 4 - AUG - 1999 5 - AUG - 1999 6 - AUG - 1999 6 - AUG - 1999 9 - AUG - 1999 1 - AUG - 1999	7 - AUG - 1999 8 - AUG - 1999 0 - AUG - 1999 0 - AUG - 1999 3 - AUG - 1999 5 - AUG - 1999 6 - AUG - 1999 7 - AUG - 1999 1 - SEP - 1999 1 - SEP - 1999
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RESULT 10 AAB82980

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28.6%;
                                                                                                                                                           ABB59430 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
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Best Local Similarity
Matches 167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL03533
                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                            pharmaceutical
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11-JUL-2000;
                                                                                                                                                                                                                          26-MAR-2002
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                                                                                                                                                                                           ABB59430;
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                                                                                                                                             ABB59430
                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing secretion of heterologous proteins e.g. lipase and cellulase in eukaryotic cells useful in industry to increase production and facilitate purification, by inducing an elevated unfolded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIFGIFDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 LQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKYSDFQGPIYG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 STAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ail---ndp----kyee---evsg 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 VNGSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGIYLCSPKTDKTSEDDENAELRYGLSAMQGWRDSMEDAHKAILNV---DKNTST---- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphatase that dephosphorylates IREI protein and regulates the unfolded protein response (UPR). The invention provides methods for increasing the secretion of a heterologous protein in a cell by inducing an elevated UPR. This can be achieved by modulating the activity of HACI (or hacA), PTC2/B or IREI in the cell. The cell from which the protein is secreted can be any cell having an UPR, such as mammalian cells, insect cells, yeast and filamentous fungi. The protein of interest can be any secreted protein such as a therapeutic protein or an industrial enzyme, e.g. lipsse, cellulase, endoglucanase-H, protease, carbohydratase, reductase, oxidase, isomerase, transferase, kinase, phosphatase, reductase, oxidase, glucoamylase, lignocellulose hemicellulase, pectinase and ligninase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is that of Trichoderma reesei PTC2, a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 sffgvfdghggdkvalfagenihnivfkqesfksgdyagglkdgflatdr------
                                                                                                                          phosphatase; unfolded protein response; protein secretion
                                                                                             Trichoderma reesei PTC2, involved in unfolded protein response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 438;
                                                                                                                                                                                                                                                                                                                                                        Saloheimo MLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
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                                                                                                                                                                                                                                                                                                                                                        Valkonen MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.5%; Score 669.5;
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AA.
AAB82980 standard; Protein; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 66; Fig 25; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                      Wang H,
                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09401.
                                                                                                                                                                                                                                                                                         24-MAR-2000; 2000US-0534692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.18;
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                        Ward M,
                                                                                                                                                                                                                                                                                                                        (GEMV ) GENENCOR INT
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-626252/72
                                                                                                                                                           Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Mismatches 116; Indels 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 5082; 21pp + Sequence Listing; English.
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                                                                                           245 qavvefvrrgiaakqdldkicenmmdnclasnsetggvgcdnmtmvii
                                                            293 QAVVDFVKSRLPTTKTLSSLCEEILDYCLSPTTRQ-QEGCDNMSIIIV
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Pred. No. 5.3e-52;
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EP1033405-A2
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Claim 8;
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                                                                                                                                                                                DKQVVTCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVKSRLPTTKTLSSLCEEI 316
                                                                                                  skneftnsstskeferninssqddeftdddadyeendnykspdtssaessdctendddqd 358
                                                                                                                                                                                                                                                                                                                                                                                         /..... "protein sequence given in the specification" 1..546 /note= "protein decoded by assers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human protein phosphatase polypeptide – useful in treatment of leukaemia, breast, brain and prostate cancer, epilepsy
                                                               239 sntttsindlstknaalkddsvndqnegsngtdfkhtlvsssnkklfatgsndmtelngs
                                                                                                                   ---GPIYGSTAVVALIRGNKLFVANAGDSRCIM
                                                                                                                                                 SRRGEAVNLSIDHKPNLEHERKRIESAGGFVH-GGRVNGSLNLTRAIGDMEFKGRPDLPP
                                                                                                                                                          rgrraaalaaeatnkavmdpsakpdgsstsaaaaaalsadgvansrnpsnvvnpmagad
                                                    ------AREDDE-----SDYSYAVLTESNDSNLAT------
                                                                                                                                                                                                                                                                                                                                   Human, MP-19; serine-threonine phosphatase; cancer; diagnosis;
phosphorylation dependent disease; leukaemia; breast; brain;
prostate; epilepsy; fatty acid; cholesterol.
                      - OLDKLGNGNSSSN-
                                                                                                                                                                                                                         LDYCLSPTTR-QQEGCDNMSIIIVQPK-----QSGVAASSSTD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                                                   Human MP-19 full length protein sequence.
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N-PSDB; AAV66512.
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                                                   The present sequence represents full length human MP-19, which is a serine/threonine phosphatase derived from human placenta. The nucleic acid sequence encodes a human protein phosphatase of the protein serine/threonine phosphatase family and is of the PP2C class which are regulate in the regulation of fatty acid and cholesterol biosynthesis. The MP-19 protein is useful in the treatment of leukaemia, brain, prostate and breast cancer, Alzheimer's, Huntington's or Parkinson's diseases, epilepsy, reproductive disorders and regulation of spermatogenesis or maturation of mammalian germ cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKEL---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              grptededekekvadeddvdneeaallheeatmtieelltryggnchkgpphsksgggtg 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 TCCPDVVEVDLGPGDEFIVLACDGIWDVMSSQAVVDFVKSRLP-----TTKTLSSLCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 546;
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; Pred. No. 5.9e-51;
60; Mismatches 112;
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Page 12; 15pp; English.
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Best Local Similarity 32.7
Matches 165; Conservative
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PR 25-FPP-2000, 2000EP-0201439.

PR 25-FPP-2000, 2000EP-0201439.

PR 25-FPP-2000, 2000EP-0201439.

PR 25-FPP-1999, 9908-0122186.

PR 25-WR-1999, 9908-012284.

PR 25-WR-1999, 9908-012284.

PR 25-WR-1999, 9908-012284.

PR 21-WR-1999, 9908-012824.

PR 21-WR-1999, 9908-012824.

PR 21-WR-1999, 9908-012824.

PR 21-WR-1999, 9908-013824.

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PR 21-WR-1999, 9908-013828.

PR 21-WR-1999, 9908-013829.

PR 21-WR-1999, 9908-013828.

PR 21-WR-1999, 9908-013845.

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990S-0144632 990S-0144632 990S-0145084 990S-0145086 990S-0145086 990S-0145089 990S-0145192 990S-0145192 990S-0145192 990S-0145193 990S-0145193 990S-0145193 990S-0145193 990S-0145193 990S-0145318 990S-0145318 990S-0147303 990S-0149368 990S-0149368

02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 13-JUL-1999; 13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 24-JUL-1999; 25-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 27-JUL-1999; 28-JUL-1999; 28

9905-0150566 9905-0150884 9905-0151065 9905-0151065 9905-0151303 9905-0151303 9905-01513303 9905-0153363 9905-0153758 9905-0153758 us-09-828-302-14.rag

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
     Arabidopsis thaliana protein fragment SEQ ID NO: 6060.
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990S-0132048.
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                                                                                Arabidopsis thaliana
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05 - MAY - 1999;
06 - MAY - 1999;
06 - MAY - 1999;
07 - MAX - 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.2%; Score 627; DB 21; Length 258; Best Local Similarity 49.2%; Pred. No. 6.4e-50; Matches 125; Conservative 43; Mismatches 76; Indels 1
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